

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Escobedo, Jaime
Quianjin, Hu
Garcia, Pablo
Williams, Lewis T.
Kothakota, Srinivas
- (ii) TITLE OF THE INVENTION: Secreted Human Proteins
- (iii) NUMBER OF SEQUENCES: 38
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Banner & Witcoff
(B) STREET: 1001 G Street, NW
(C) CITY: Washington
(D) STATE: DC
(E) COUNTRY: USA
(F) ZIP: 20001
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE: 11-DEC-1997
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 60/032757
(B) FILING DATE: 11-DEC-1996
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Kagan, Sarah A
(B) REGISTRATION NUMBER: 32141
(C) REFERENCE/DOCKET NUMBER: 2441.39505
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 202-508-9100
(B) TELEFAX: 202-508-9299
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2063 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCGGCA	CGAGGCCTCA	GTCTTCCAGG	GCGGCGGTGG	GTGTCCGCTT	CTCTCTGCTC	60
TTCGACTGCA	CCGCACTCGC	GCGTGACCCT	GACTCCCCCT	AGTCAGCTCA	GCGGTGCTGC	120
CATGGCGTGG	CGGCGGCGCG	AAGCCGGCGT	CGGGGCTCGC	GGCGTGTGG	CTCTGGCGTT	180
GCTCGCCCTG	GCCCTGTGCG	TGCCCCGGGC	CCGGGGCCGG	GCTCTCGAGT	GGTTCTCGGC	240
CGTGGTAAAC	ATCGAGTACG	TGGACCCGCA	GACCAACCTG	ACGGTGTGGA	GCGTCTCGGA	300
GAGTGGCCGC	TTCGGCGACA	GCTCGCCCAA	GGAGGGCGCG	CATGGCCTGG	TGGGCGTCCC	360
GTGGGCGCCC	GGCGGAGACC	TCGAGGGCTG	CGCGCCCAC	ACGCGCTTCT	TCGTGCCCCA	420
GCCCCGCGGC	CGAGGGGCCG	CGCCCTGGGT	CGCCCTGGTG	GCTCGTGGGG	GCTGCACCTT	480
CAAGGACAAG	GTGCTGGTGG	CGGCGCGGAG	GAACGCCTCG	GCCGTCGTCC	TCTACAATGA	540
GGAGCGCTAC	GGGAACATCA	CCTTGCCCAT	GTCTCACGCG	GGAACAGGAA	ATATAGTGGT	600
CATTATGATT	AGCTATCCAA	AAGGAAGAGA	AATTTTGGAG	CTGGTGCAAA	AAGGAATTCC	660
AGTAACGATG	ACCATAGGGG	TTGGCACCCG	GCATGTACAG	GAGTTCATCA	GCGGTCAGTC	720
TGTGGTGTIT	GTGGCCATTG	CCTTCATCAC	CATGATGATT	ATCTCGTTAG	CCTGGCTAAT	780
ATTTTACTAT	ATACAGCGTT	TCCTATATAC	TGGCTCTCAG	ATTGGAAGTC	AGAGCCATAG	840
AAAAGAAACT	AAGAAAGTTA	TTGGCCAGCT	TCTACTTCAT	ACTGTAAAGC	ATGGAGAAAA	900
GGGAATTGAT	GTTGATGCTG	AAAATTGTGC	AGTGTGTATT	GAAAAATTCA	AAGTAAAGGA	960
TATTATTAGA	ATTCTGCCAT	GCAAGCATAT	TTTTCATAGA	ATATGCATTG	ACCCATGGCT	1020
TTTGGATCAC	CGAACATGTC	CAATGTGTAA	ACTTGATGTC	ATCAAAGCCC	TAGGATATTG	1080
GGGAGAGCCT	GGGGATGTAC	AGGAGATGCC	TGCTCCAGAA	TCTCCTCCTG	GAAGGGATCC	1140
AGCTGCAAA	TTGAGTCTAG	CTTTACCAGA	TGATGACGGA	AGTGATGACA	GCAGTCCACC	1200
ATCAGCCTCC	CCTGCTGAAT	CTGAGCCACA	GTGTGATCCC	AGCTTTAAAG	GAGATGCAGG	1260
AGAAAAATACG	GCATTGCTAG	AAGCCGGCAG	GAGTGACTCT	CGGCATGGAG	GACCCATCTC	1320
CTAGCACACG	TGCCCCACTGA	AGTGGCACCA	ACAGAAGTTT	GGCTTGAAGT	AAAGGACATT	1380
TTATTTTTTT	TACTTTAGCA	CATAATTTGT	ATATTTGAAA	ATAATGTATA	TTATTTTACC	1440
TATTAGATTC	TGATTTGATA	TACAAAGGAC	TAAGATATTT	TCTTCTTGAA	GAGACTTTTC	1500
GATTAGTCCT	CATATATTTA	TCTACTAAAA	TAGAGTGTTT	ACCATGAACA	GTGTGTTGCT	1560
TCAGACTATT	ACAAAGACAA	CTGGGGCAGG	TACTCTAATA	TAAAGGACAG	GTGGTGTTC	1620
TAAATAATTG	GCTGCTATGG	TTCTGTAAAA	ACCAGTTAAT	TCTATTTTTC	AAGGTTTTTG	1680
GCAAAGCACA	TCAATGTTAG	ACTAGTTGAA	GTGGAATTGT	ATAATTCAAT	TCGATAATTG	1740
ATCTCATGGG	CTTTCCCTGG	AGGAAAGGTT	TTTTTTGTTG	TTTTTTTTTT	AAGAACTTGA	1800
AACTTGTAAG	CTGAGATGTC	TGTAGCTTTT	TTGCCATCT	GTAGTGATG	TGAAGATTTC	1860
AAAACCTGAG	AGCACTTTTT	CTTTGTTTGT	AATTATGAGA	AAGGCACTAG	ATGACTTTAG	1920
GATTTGCATT	TTTCCCTTTA	TTGCCTCATT	TCTTGTCACG	CCTTGTTGGG	GAGGGAAATC	1980
TGTTTATTTT	TTCCTACAAA	TAAAAAGCTA	AGATTCTATA	TCGCAAAAAA	AAAAAAAAAA	2040
AAAAAAAAAA	TTCCTGCGGC	CGC				2063

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1328 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAATTCGGCA	CGAGGTAGGC	AAGGGATAAA	AAGGCACCTA	AGGCCCTTTT	GCAATAAGAA	60
GCCAGATGGA	TAAAGGAAGT	GCTGGTCACC	CTGGAGGTGT	ACTGGTTTGG	GGAAGGTCCC	120

CGGCCCCCAC	AGCCCTCTGG	GGAGCCTCAC	CCTGGCTCTC	CCCACTCACC	TCAGCCCTCA	180
GGCAGCCCCT	CCACAGGGCC	CCTCTCCTGC	CTGGACAGCT	CTGCTGGTCT	CCCCGTCCCC	240
TGGAGAAGAA	CAAGGCCATG	GGTCGGCCCC	TGCTGCTGCC	CCTGCTGCTC	CTGCTGCAGC	300
CGCCAGCATT	TCTGCAGCCT	GGTGGCTCCA	CAGGATCTGG	TCCAAGCTAC	CTTTATGGGG	360
TCACTCAACC	AAAACACCTC	TCAGCCTCCA	TGGGTGGCTC	TGTGGAAATC	CCCTTCTCCT	420
TCTATTACCC	CTGGGAGTTA	GCCATAGTTC	CCAACGTGAG	AATATCCTGG	AGACGGGGCC	480
ACTTCCACGG	GCAGTCCTTC	TACAGCACAA	GGCCGCCTTC	CATTCAACAAG	GATTATGTGA	540
ACCGGCTCTT	TCTGAACTGG	ACAGAGGGTC	AGGAGAGCGG	CTTCCTCAGG	ATCTCAAACC	600
TGCGGAAGGA	GGACCAGTCT	GTGTATTTCT	GCCGAGTCGA	GCTGGACACC	CGGAGATCAG	660
GGAGGCAGCA	GTTGCAGTCC	ATCAAGGGGA	CCAAACTCAC	CATCACCAG	GCTGTCACAA	720
CCACCACCAC	CTGGAGGGCC	AGCAGCACAA	CCACCATAGC	CGGCCTCAGG	GTACACAGAA	780
GCAAAGGGCA	CTCAGAATCA	TGGCACCTAA	GTCTGGACAC	TGCCATCAGG	GTTGCATTGG	840
CTGTCGCTGT	GCTCAAAACT	GTCATTTTGG	GACTGCTGTG	CCTCCTCCTC	CTGTGGTGGA	900
GGAGAAGGAA	AGGTAGCAGG	GCGCCAAGCA	GTGACTTCTG	ACCAACAGAG	TGTGGGGAGA	960
AGGGATGTGT	ATTAGCCCCG	GAGGACGTGA	TGTGAGACCC	GCTTGTGAGT	CCTCCACACT	1020
CGTTCCCCAT	TGGCAAGATA	CATGGAGAGC	ACCCTGAGGA	CCTTTAAAAG	GCAAAGCCGC	1080
AAGGCAGAAG	GAGGCTGGGT	CCCTGAATCA	CCGACTGGAG	GAGAGTTACC	TACAAGAGCC	1140
TTCATCCAGG	AGCATCCACA	CTGCAATGAT	ATAGGAATGA	GGTCTGAACT	CCACTGAATT	1200
AAACCACTGG	CATTTGGGGG	CTGTTTATTA	TAGCAGTGCA	AAGAGTTCCT	TTATCCTCCC	1260
CAAGGATGGA	AAAATACAAT	TTATTTTGCT	TACCATAAAA	AAAAAAAAAA	AAAAATTCCT	1320
GCGGCCCGC						1328

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1689 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTGCGCA	CGAGGGCAAG	ATTGATACA	AAACCAATGA	ACCTGTGTGG	GAGGAAAAC	60
TCACTTTCTT	CATTCAACA	CCCAAGCGCC	AGGACCTTGA	AGTTGAGGTC	AGAGACGAGC	120
AGCACCAGTG	TTCCCTGGGG	AACCTGAAGG	TCCCCCTCAG	CCAGCTGCTC	ACCAGTGAGG	180
ACATGACTGT	GAGCCAGCGC	TTCCAGCTCA	GTAACCTCGG	TCCAAACAGC	ACCATCAAGA	240
TGAAGATTGC	CCTGCGGGTG	CTCCATCTCG	AAAAGCGAGA	AAGGCCTCCA	GACCACCAAC	300
ACTCAGCTCA	AGTCAAACGT	CCCTCTGTGT	CCAAAGAGGG	GAGGAAAACA	TCCATCAAAT	360
CTCATATGTC	TGGGTCTCCA	GGCCCTGGTG	GCAGCAACAC	AGCTCCATCC	ACACCAGTCA	420
TTGGGGGCG	TGATAAGCCT	GGTATGGAAG	AAAAGGCCCA	GCCCCCTGAG	GCCGGCCCTC	480
AGGGGCTGCA	CGACCTGGGC	AGAAGCTCCT	CCAGCCTCCT	GGCCTCCCCA	GGCCACATCT	540
CAGTCAAGGA	GCCGACCCCC	AGCATCGCCT	CGGACATCTC	GCTGCCCATC	GCCACCCAGG	600
AGCTGCGGCA	AAGGCTGAGG	CAGCTGGAAG	ACGGGACGAC	CCTGGGACAG	TCTCCACTGG	660
GGCAGATCCA	GCTGACCATC	CGGCACAGCT	CGCAGAGAAA	CAAGCTTATC	GTGGTCGTGC	720
ATGCCTGCAG	AAACCTCATT	GCCTTCTCTG	AAGACGGCTC	TGACCCCTAT	GTCCGCATGT	780
ATTTATTACC	AGACAAGAGG	CGGTCAGGAA	GGAGGAAAAC	ACACGTGTCA	AAGAAAACAT	840
TAAATCCAGT	GTTTGATCAA	AGCTTTGATT	TCAGTGTTTC	GTTACCAGAA	GTGCAGAGGA	900
GAACGCTCGA	CGTTGCCGTG	AAGAACAGTG	GCGGCTTCCT	GTCCAAAGAC	AAAGGGCTCC	960
TTGGCAAAGT	ATTGGTTGCT	CTGGCATCTG	AAGAACCTGC	CAAAGGCTGG	ACCCAGTGGT	1020
ATGACCTCAC	GGAAGATGGG	ACGAGGCCTC	AGGCGATGAC	ATAGCCGCAG	CAGGCAGGAG	1080
GCGTCTCTT	CAGCGTAGCT	CTCCACCTCT	ACCCGGAACA	CACCTCTCA	CAGACGTACC	1140
AATGTTATTT	TTATAATTTT	ATGGATTTAG	TTATACATAC	CTTAATAGTT	TTATAAAATT	1200
GTTGACATTT	CAGGCAAATT	TGGCCAATAT	TATCATTGAA	TTTTCTGTGT	TGGATTTCCT	1260
CTAGGATTTT	GCCAGTTCCT	ACAACGTGCA	GTAGGGCGGC	GGTAGCTCTT	GTGTCTGTGG	1320
ACTCTGCTCA	GCTGTGTCCG	TAGGAGTCGG	ATGTGTCTGT	GCTTTATTAT	GGCCTTGTTT	1380
ATATATCACT	GAGGTATACT	ATGCCATGTA	AATAGACTAT	TTTTTATAAT	CTTAACATGC	1440

TGGTTTAAAT	TCAGAAGGAA	ATAGATCAAG	GAAATATATA	TATTTTCTTC	TAAAACTTAT	1500
TAAATTCGTG	TGACAAATAA	TCATTTTCAT	CTTGGCAGCA	AAAAGTTCTC	AGTGACCTAT	1560
TTTGTGGTGT	TTCTTTTTGA	AAAGAAAAGC	TGAAATATTA	TTAAATGCTA	GTATGTTTCT	1620
GCCCATTATG	AAAGATGAAA	TAAAGTATTC	AAAAATATTAA	AAAAAAAAAA	AAAAAATTCC	1680
TGCGGCCCGC						1689

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTCGGCA	CGAGGAGCAG	ATCTGCAAGA	GTTTCGTTTA	TGGAGGCTGC	TTGGGCAACA	60
AGAACAACCTA	CCTTCGGGAA	GAAGAGTGCA	TTCTAGCCTG	TCGGGGTGTG	CAAGGTGGGC	120
CTTTGAGAGG	CAGCTCTGGG	GCTCAGGCGA	CTTTCCCCCA	GGGCCCCCTCC	ATGGAAAGGC	180
GCCATCCAGT	GTGCTCTGGC	ACCTGTCAGC	CCACCCAGTT	CCGCTGCAGC	AATGGCTGCT	240
GCATCGACAG	TTTCCTGGAG	TGTGACGACA	CCCCCAACTG	CCCCGACGCC	TCCGACGAGG	300
CTGCCTGTGA	AAAATACACG	AGTGGCTTTG	ACGAGCTCCA	GCGCATCCAT	TTCCCCAGCG	360
ACAAAGGGCA	CTGCGTGGAC	CTGCCAGACA	CAGGACTCTG	CAAGGAGAGC	ATCCCGCGCT	420
GGTACTACAA	CCCCTTCAGC	GAACACTGCG	CCCGCTTTAC	CTATGGTGGT	TGTTACGGCA	480
ACAAGAACAA	CTTTGAGGAA	GAGCAGCAGT	GCCTCGAGTC	TTGTCGCGGC	ATCTCCAAGA	540
AGGATGTGTT	TGGCCTGAGG	CGGGAAATCC	CCATTCCCAG	CACAGGCTCT	GTGGAGATGG	600
CTGTGCGAGT	GTTCTTGTC	ATCTGCATTG	TGGTGGTGGT	AGCCATCTTG	GGTTACTGCT	660
TCTTCAAGAA	CCAGAGAAAG	GACTTCCACG	GACACCACCA	CCACCCACCA	CCCACCCCTG	720
CCAGCTCCAC	TGTCTCCACT	ACCGAGGACA	CGGAGCACCT	GGTCTATAAC	CACACCACGC	780
GGCCCCCTCTG	AGCCTGGGTC	TCACCGGCTC	TCACCTGGCC	CTGCTTCCTG	CTTGCCAAGG	840
CAGAGGCCTG	GGCTGGGAAA	AACTTTGGAA	CCAGACTCTT	GCCTGTTTCC	CAGGCCCACT	900
GTGCCTCAGA	GACCAGGGCT	CCAGCCCCCTC	TTGGAGAAGT	CTCAGCTAAG	CTCACGTCCT	960
GAGAAAGCTC	AAAGGTTTGG	AAGGAGCAGA	AAACCCTTGG	GCCAGAAGTA	CCAGACTAGA	1020
TGGACCTGCC	TGCATAGGAG	TTTGGAGGAA	GTTGGAGTTT	TGTTTCCTCT	GTTCAAAGCT	1080
GCCTGTCCCT	ACCCCATGGT	GCTAGGAAGA	GGAGTGGGGT	GGTGTGAGAC	CCTGGAGGCC	1140
CCAACCCTGT	CCTCCCGAGC	TCCTCTTCCA	TGCTGTGCGC	CCAGGGCTGG	GAGGAAGGAC	1200
TTCCCTGTGT	AGTTTGTGCT	GTAAAGAGTT	GCTTTTTGTT	TATTTAATGC	TGTGGCATGG	1260
GTGAAGAGGA	GGGGAAGAGG	CCTGTTTGGC	CTCTCTATCC	TCTCTTCCTC	TTCCCCCAAG	1320
ATTGAGCTCT	CTGCCCTTGA	TCAGCCCCAC	CCTGGCCTAG	ACCAGCAGAC	AGAGCCAGGA	1380
GAAGCTCAGC	TGCATTCCGC	AGCCCCCACC	CCCAAGGTTT	TCCAACATCA	CAGCCCAGCC	1440
CGCCCCTGCG	GTAATAAAAG	TGGTTTGTGG	AAAAAAAAAA	AAAAAAAAAA	AAGTCCTGCG	1500
GCCGC						1505

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2002 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCGGCA	CGAGGGCCAT	GGCCGGGCTA	TCCCGCGGGT	CCGCGCGCGC	ACTGCTCGCC	60
GCCCTGCTGG	CGTCGACGCT	GTTGGCGCTG	CTCGTGTCGC	CCGCGCGGGG	TCGCGGCGGC	120

CGGGACCACG	GGGACTGGGA	CGAGGCCTCC	CGGCTGCCGC	CGCTACCACC	CCGCGAGGAC	180
GCGGCGCGCG	TGGCCCGCTT	CGTGACGCAC	GTCTCCGACT	GGGGCGCTCT	GGCCACCATC	240
TCCACGCTGG	AGGCGGTGCG	CGGCCGGCCC	TCGCCGACG	TCCTCTCGCT	CAGCGACGGG	300
CCCCCGGGCG	CGGGCAGCGG	CGTGCCCTAT	TTCTACCTGA	GCCCGCTGCA	GCTCTCCGTG	360
AGCAACCTGC	AGGAGAATCC	ATATGCTACA	CTGACCATGA	CTTTGGCACA	GACCAACTTC	420
TGCAAGAAAC	ATGGATTGGA	TCCACAAAGT	CCCCTTTGTG	TTACATAAT	GCTGTCAGGA	480
ACTGTGACCA	AGGTGAATGA	AACAGAAATG	GATATTGCAA	AGCATTCGTT	ATTCATTCTGA	540
CACCCTGAGA	TGAAAACCTG	GCCTTCCAGC	CATAATTGGT	TCTTTGCTAA	GTTGAATATA	600
ACCAATATCT	GGGTCCTGGA	CTACTTTGGT	GGACCAAAAA	TCGTGACACC	AGAAGAATAT	660
TATAATGTCA	CAGTTCAGTG	AAGCAGACTT	TGGTGAATTT	AGCAACACTT	ATGAAGTTTC	720
TTAAAGTGGC	TCATACACAC	TTAAAAGGCT	TAATGTTTCT	CTGGAAAGCG	TCCCAGAATA	780
TTAGCCAGTT	TTCTGTCACA	TGCTGGTTTG	TTTGCTTGCT	TGTTTACTTG	CTTGTTTACC	840
AATAGAGTTG	ACCTGTTATT	GGATTTCCCTG	GAAGATGTGG	TAGCTACTTT	TTTCCTATTT	900
TGAAGCCATT	TTCTGTAGAGA	AATATCCTTC	ACTATAATCA	AATAAGTTTT	GTCCCATCAA	960
TTCCAAAGAT	GTTTCCAGTG	GTGCTCTTGA	AGAGGAATGA	GTACCAGTTT	TAAATTGCCC	1020
ATTGGCATT	GAAGGTAGTT	GAGTATGTGT	TCTTTATTCC	TAGAAGCCAC	TGTGCTTGGT	1080
AGAGTGCATC	ACTCACCACA	GCTGCCTCTT	GAGCTGCCTG	AGCCTGGTGC	AAAAGGATTG	1140
GCCCCCATT	TGGTGCTTCT	GAATAAATCT	TGCCAAGATA	GACAAACAAT	GATGAAACTC	1200
AGATGGAGCT	TCCTACTCAT	GTTGATTTAT	GTCTCACAAT	CCTGGGTATT	GTTAATTCAA	1260
CATAGGGTGA	AACTATTTCT	GATAAAGAAC	TTTTGAAAAA	CTTTTATAC	TCTAAAGTGA	1320
TACTCAGAAC	AAAAGAAAGT	CATAAACTC	CTGAATTTAA	TTCCCCACC	TAAGTCGAGA	1380
CAGTATTATC	AAAACACATG	TGCACACAGA	TTATTTTTTG	GCTCCAAAAC	TGGATTGCAA	1440
AAGAAAGAGG	AGAGATATTT	TGTGTGTTCC	TGGTATTCTT	TTATAAGTAA	AGTTACCCAG	1500
GCATGGACCA	GCTTCAGCCA	GGGACAAAAT	CCCCTCCCAA	ACCACTCTCC	ACAGCTTTTT	1560
AAAAATACTT	CTACTCTTAA	CAATTACCTA	AGGTTCCCTC	AAACCCCCC	AACTCTTAAT	1620
AGCTTCTAGT	GCTGCTACAA	TCTAAGTCAG	GTCACCAGAG	GGAAGAGAAC	ATGGCATTA	1680
AAGAATCACA	TCTTCAGAAG	AGAAGACACT	AATATTATTA	CCCATATACA	TGATTTCAGA	1740
AGATGACATA	AGATTCTCT	TAAAGAGGAA	ATGTCAGGAA	TCAAGCCACT	GAATCCTTAA	1800
AGAGAAAAGT	TGAATATGAG	TCATTGTGTC	TGAAAAGTGC	AAAGTGAAGT	TAACTGAGAT	1860
CCAGCAAACA	GGTTCTGTTT	AAGAAAAATA	ATTTTATACTA	AATTTAGTAA	AATGGACTTC	1920
TTATTCAAAG	CATCAATAAT	TAAAAGAATT	ATTTTAAAAA	AAAAAATAAA	AAAAAATAAA	1980
AAAAAATAAT	TCCTGCGGCC	GC				2002

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAATTCGGCA	CGAGGGCCAC	GACTCTGCTG	GCATTTCTTC	TATAGCCACT	GGAATCTGAT	60
CCTGATTGTC	TTCCACTACT	ACCAGGCCAT	CACCACTCCG	CCTGGGTACC	CACCCAGGG	120
CAGGAATGAT	ATCGCCACCG	TCTCCATCTG	TAAGAAGTGC	ATTTACCCCA	AGCCAGCCCCG	180
AACACACCAC	TGCAGCATCT	GCAACAGGTG	TGTGCTGAAG	ATGGATCACC	ACTGCCCTG	240
GCTAAACAAT	TGTGTGGGCC	ACTATAACCA	TCGGTACTTC	TTCTCTTTCT	GCTTTTTTCAT	300
GACTCTGGGC	TGTGTCTACT	GCAGCTATGG	AAGTTGGGAC	CTTTTCCGGG	AGGCTTATGC	360
TGCCATTGAG	AAAATGAAAC	AGCTCGACAA	GAACAACTA	CAGGCGGTTG	CCAACCAGAC	420
TTATCACCAG	ACCCACCCAC	CCACCTTCTC	CTTTCGAGAA	AGGATGACTC	ACAAGAGTCT	480
TGCTACCTC	TGGTTCCTGT	GCAGTTCTGT	GGCACTTGCC	CTGGGTGCCC	TAACTGTATG	540
GCATGCTGTT	CTCATCAGTC	GAGGTGAGAC	TAGCATCGAA	AGGCACATCA	ACAAGAAGGA	600
GAGACGTCGG	CTACAGGCCA	AGGGCAGAGT	ATTTAGGAAT	CCTTACAAC	ACGGCTGCTT	660
GGACAACTGG	AAGGTATTCC	TGGGTGTGGA	TACAGGAAGG	CACTGGCTTA	CTCGGGTGCT	720
CTTACCTTCT	ACTCACTTGC	CCCATGGGAA	TGGAATGAGC	TGGGAGCCCC	CTCCCTGGGT	780

GACTGCTCAC	TCAGCCTCTG	TGATGGCAGT	GTGAGCTGGA	CTGTGTCAGC	CACGACTCGA	840
GCACTCATTC	TGCTCCCTAT	GTTATTTCAA	GGGCCTCCAA	GGGCAGCTTT	TCTCAGAATC	900
CTTGATCAAA	AAGAGCCAGT	GGGCCTGCCT	TAGGGTACCA	TGCAGGACAA	TTCAAGGACC	960
AGCCTTTTTTA	CCACTGCAGA	AGAAAAGACAC	AATGTGGAGA	AATCTTAGGA	CTGACATCCC	1020
TTTACTCAGG	CAAACAGAAG	TTCCAACCCC	AGACTAGGGG	TCAGGCAGCT	AGCTACCTAC	1080
CTTGCCCACT	GCTGACCCGG	ACCTCCTCCA	GGATACAGCA	CTGGAGTTGG	CCACCACCTC	1140
TTCTACTTGC	TGTCTGAAAA	AACACCTGAC	TAGTACAGCT	GAGATCTTGG	CTTCTCAACA	1200
GGGCAAAGAT	ACCAGGCCTG	CTGCTGAGGT	CACTGCCACT	TCTCACATGC	TGCTTAAGGG	1260
AGCACAAATA	AAGGTATTCG	ATTTTAAAAA	AAAAAAAAAA	AAAAAAAAAT	TCCTGCGGCC	1320
GC						1322

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAATTCGGCA	CGAGGAGCCT	GCCTTCATCT	AGGATGGCTC	CTCTGGGCAT	GCTGCTTGGG	60
CTGCTGATGG	CCGCCTGCTT	CACCTTCTGC	CTCAGTCATC	AGAACCTGAA	GGAGTTTGCC	120
CTGACCAACC	CAGAGAAGAG	CAGCACCAAA	GAAACAGAGA	GAAAAGAAAC	CAAAGCCGAG	180
GAGGAGCTGG	ATGCCGAAGT	CCTGGAGGTG	TTCCACCCGA	CGCATGAGTG	GCAGGCCCTT	240
CAGCCAGGGC	AGGCTGTCCC	TGCAGGATCC	CACGTACGGC	TGAATCTTCA	GAAGGGGAA	300
AGAGAGGCAA	AACTCCAATA	TGAGGACAAG	TTCCGAAATA	ATTGAAAGG	CAAAAGGCTG	360
GATATCAACA	CCAACACCTA	CACATCTCAG	GATCTCAAGA	GTGCACTGGC	AAAATTCAG	420
GAGGGGGCAG	AGATGGAGAG	TTCAAAGGAA	GACAAGGCAA	GGCAGGCTGA	GGTAAAGCGG	480
CTCTTCCGCC	CCATTGAGGA	ACTGAAGAAA	GACTTTGATG	AGCTGAATGT	TGTCATTGAG	540
ACTGACATGC	AGATCATGGT	ACGGCTGATC	AACAAGTTCA	ATAGTTCCAG	CTCCAGTTTG	600
GAAGAGAAGA	TTGCTGCGCT	CTTTGATCTT	GAATATTATG	TCCATCAGAT	GGACAATGCG	660
CAGGACCTGC	TTTCCTTTGG	TGGTCTTCAA	GTGGTGATCA	ATGGGCTGAA	CAGCACAGAG	720
CCCCTCGTGA	AGGAGTATGC	TGCGTTTGTG	CTGGGCGCTG	CCTTTTCCAG	CAACCCCAAG	780
GTCCAGGTGG	AGGCCATCGA	AGGGGGAGCC	CTGCAGAAGC	TGCTGGTCAT	CCTGGCCACG	840
GAGCAGCCGC	TCACTGCAAA	GAAGAAGGTC	CTGTTTGCAC	TGTGCTCCCT	GCTGCGCCAC	900
TTCCCTATAG	CCCAGCGGCA	GTTCTTGAAG	CTCGGGGGGC	TGCAGGTCCT	GAGGACCTG	960
GTGCAGGAGA	AGGGCACGGA	GGTGCTCGCC	GTGCGCGTGG	TCACACTGCT	CTACGACCTG	1020
GTCACGGAGA	AGATGTTTCG	CGAGGAGGAG	GCTGAGCTGA	CCCAGGAGAT	GTCCCCAGAG	1080
AAGCTGCAGC	AGTATCGCCA	GGTACACCTC	CTGCCAGGCC	TGTGGGAACA	GGGCTGGTGC	1140
GAGATCACGG	CCCACCTCCT	GGCGCTGCCC	GAGCATGATG	CCCGTGAGAA	GGTGCTGCAG	1200
ACACTGGGCG	TCCTCCTGAC	CACCTGCCGG	GACCGCTACC	GTCAGGACCC	CCAGCTCGGC	1260
AGGACACTGG	CCAGCCTGCA	GGCTGAGTAC	CAGGTGCTGG	CCAGCCTGGA	GCTGCAGGAT	1320
GGTGAGGACG	AGGGCTACTT	CCAGGAGCTG	CTGGGCTCTG	TCAACAGCTT	GCTGAAGGAG	1380
CTGAGATGAG	GCCCCACACC	AGGACTGGAC	TGGGATGCCG	CTAGTGAGGC	TGAGGGGTGC	1440
CAGCGTGGGT	GGGCTTCTCA	GGCAGGAGGA	CATCTTGGCA	GTGCTGGCTT	GGCCATTAAA	1500
TGGAACCTG	AAGGCCAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	1560
TTCTGCGGC	CGC					1573

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAATTCGGCA	CGAGGGGGCT	TTAAGGGACA	GCTGAGCCGG	CAGGTGGCAG	ATCAGATGTG	60
GCAGGCTGGG	AAAAGACAAG	CCTCCAGGGC	CTTCAGCTTG	TACGCCAACA	TCGACATCCT	120
CAGACCCTAC	TTTGATGTGG	AGCCTGCTCA	GGTGCGAAGC	AGGCTCCTGG	AGTCCATGAT	180
CCCTATCAAG	ATGGTCAACT	TCCCCAGAA	AATTGCAGGT	GAACCTCTATG	GACCTCTCAT	240
GCTGGTCTTC	ACTCTGGTTG	CTATCCTACT	CCATGGGATG	AAGACGTCTG	ACACTATTAT	300
CCGGGAGGGC	ACCCTGATGG	GCACAGCCAT	TGGCACCTGC	TTCGGCTACT	GGCTGGGAGT	360
CTCATCCTTC	ATTTACTTCC	TTGCCTACCT	GTGCAACGCC	CAGATCACCA	TGCTGCAGAT	420
GTTGGCACTG	CTGGGCTATG	GCCTCTTTGG	GCATTGCATT	GTCCTGTTCA	TCACCTATAA	480
TATCCACCTC	CACGCCCTCT	TCTACCTCTT	CTGGCTGTTG	GTGGGTGGAC	TGTCCACACT	540
GCGCATGGTA	GCAGTGTTGG	TGTCTCGGAC	CGTGGGCCCC	ACACAGCGGC	TGCTCCTCTG	600
TGGCACCTTG	GCTGCCCTAC	ACATGCTCTT	CCTGCTCTAT	CTGCATTTTG	CCTACCACAA	660
AGTGGTAGAG	GGGATCCTGG	ACACACTGGA	GGGCCCCAAC	ATCCCGCCCA	TCCAGAGGGT	720
CCCCAGAGAC	ATCCCTGCCA	TGCTCCCTGC	TGCTCGGCTT	CCCACCACCG	TCCTCAACGC	780
CACAGCCAAA	GCTGTTGCGG	TGACCCTGCA	GTCACACTGA	CCCCACCTGA	AATTCTTGGC	840
CAGTCCTCTT	TCCCGCAGCT	GCAGAGAGGA	GGAAGACTAT	TAAAGGACAG	TCCTGATGAC	900
ATGTTTCGTA	GATGGGGTTT	GCAGCTGCCA	CTGAGCTGTA	GCTGCGTAAG	TACCTCCTTG	960
ATGCCTGTCTG	GCACCTCTGA	AAGGCACAAG	GCCAAGAAGT	CCTGGCCAGG	ACTGCAAGGC	1020
TCTGCAGCCA	ATGCAGAAAA	TGGGTCAGCT	CCTTTGAGAA	CCCCTCCCCA	CCTACCCCTT	1080
CCTTCCTCTT	TATCTCTCCC	ACATTGTCTT	GCTAAATATA	GACTTGGTAA	TTAAATGTT	1140
GATTGAAGTC	TGGAATAAAA	AAAAAAAAAA	AATTCCTGCG	GCCGC		1185

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1226 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GAATTCGGCA	CGAGGCAAGC	CACCATCTTC	CTTCGGCCTG	CACCCCTTTA	AAGGCACCCA	60
GACCCCTCTG	GAAAAAGATG	AACTGAAGCC	CTTTGACATC	CTCCAGCCTA	AGGAGTACTT	120
CCAGCTCAGC	CGCCACACGG	TCATTAAGAT	GGGAAGTGAG	AACGAGGCC	TGGATCTCTC	180
CATGAAGTCA	GTGCCCTGGC	TCAAGGCTGG	TGAAGTCAGT	CCCCCAATCT	TCCAGGAAGA	240
TGCAGCCCTA	GACCTGTGAG	TGGCAGCCCA	CCGGAATCC	GAGCCTCCCC	CTGAGACACT	300
GTATGACAGT	GGTGCATCAG	TGGACAGCTC	AGGTCACACA	GTGATGGAGA	AACTTCCCAG	360
TGGCATGGAA	ATTTCTTTTG	CCCCTGCCAC	GTCCCATGAG	GCCCCAGCCA	TGATGGATAG	420
TCACATCAGC	AGCAGTGATG	CTGCTACCGA	GATGCTCAGC	CAGCCCAACC	ACCCAGCGG	480
CGAAGTCAAG	GCTGAAAATA	ACATTGAGAT	GGTGGGCGAG	TCCCAGGCGG	CCAAGGTCAT	540
TGTCTCTGTC	GAAGATGCTG	TGCCTACCAT	ATTCTGTGGC	AAGATCAAAG	GCCTCTCAGG	600
GGTGTCCACC	AAAAACTTCT	CCTTCAAAAG	AGAAGACTCC	GTGCTTCAGG	GCTATGACAT	660
CAACAGCCAA	GGGGAAGAGT	CCATGGGAAA	TGCAGAGCCC	CTTAGGAAAC	CCATCAAAAA	720
CCGGAGCATA	AAGTTAAAGA	AAGTGAAGTC	CCAGGAAGTA	CACATGCTCC	CAATCAAAAA	780
ACAACGGCTG	GCCACCTTTT	TTCCAAGAAA	GTAAATAACG	GCTTTTTTAA	ATTTGTATGA	840
TTATAATATG	GGGAAAGGTG	CATTGGTTTT	ATAAAAAGGC	ATTTAAAACA	AATTATCTTT	900
GTTAATTATT	TTGGGGAGTA	GTTGGGAAAT	GGAAAGGTGA	ATTGGCTCTA	GAGGCCCTGT	960
ATGCTAGTAT	CATTTTCTTT	TTTAATTTTT	GACTTTTCAC	AAATGAGTAA	ATAAGAGCAA	1020
CCTATTTTTT	AAGCAGATTG	CACATTTTTT	GCAGCTTTAA	TGGAATATTG	GGTGAATTAG	1080
AGGGGTAAAA	AAAGCTATTT	TCATTGCCAC	AAAGTGCTTT	GATGATGTAA	TACCTAATAA	1140
AGGGTAGGAT	GAATATTTCA	CAATAAATGT	TTGTTTGCAC	TAAAAAATAA	AAAAAATAA	1200
AAAAAATAA	AAATTCCTGC	GGCCGC				1226

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1049 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAATTCGGCA	CGAGGGCGCC	ATGGTGAAGG	TGACGTTCAA	CTCCGCTCTG	GCCCAGAAGG	60
AGGCCAAGAA	GGACGAGCCC	AAGAGCGGCG	AGGAGGCGCT	CATCATCCCC	CCCGACGCCG	120
TCGCGGTGGA	CTGCAAGGAC	CCAGATGATG	TGGTACCAGT	TGGCCAAAGA	AGAGCCTGGT	180
GTTGGTGCAT	GTGCTTTGGA	CTAGCATTTA	TGCTTGCAGG	TGTTATTCTA	GGAGGAGCAT	240
ACTTGTAACA	ATATTTTGCA	CTTCAACCAG	ATGACGTGTA	CTACTGTGGA	ATAAAGTACA	300
TCAAAGATGA	TGTCATCTTA	AATGAGCCCT	CTGCAGATGC	CCCAGCTGCT	CTCTACCAGA	360
CAATTGAAGA	AAATATTAAA	ATCTTTGAAG	AAGAAGAAGT	TGAATTTATC	AGTGTGCCTG	420
TCCCAGAGTT	TGCAGATAGT	GATCCTGCCA	ACATTGTTCA	TGACTTTAAC	AAGAAACTTA	480
CAGCCTATTT	AGATCTTAAC	CTGGATAAGT	GCTATGTGAT	CCCTCTGAAC	ACTTCCATTG	540
TTATGCCACC	CAGAAACCTA	CTGGAGTTAC	TTATTAACAT	CAAGGCTGGA	ACCTATTTGC	600
CTCAGTCCTA	TCTGATTCAT	GAGCACATGG	TTATTACTGA	TCGCATTGAA	AACATTGATC	660
ACCTGGGTTT	CTTTATTTAT	CGACTGTGTC	ATGACAAGGA	AACTTACAAA	CTGCAACGCA	720
GAGAACTAT	TAAAGGTATT	CAGAAACGTG	AAGCCAGCAA	TTGTTTCGCA	ATTTCGGCATT	780
TTGAAAACAA	ATTTGCCGTG	GAAACTTTAA	TTTGTCTTTC	AACAGTCAAG	AAAAACATTA	840
TTGAGGAAAA	TTAATATCAC	AGCATAACCC	CACCCTTTAC	ATTTTGTGTC	AGTTGATTAT	900
TTTTTAAAGT	CTTCTTTTAT	GTAAGTAGCA	AACAGGGCTT	TACTATCTTT	TCATCTCATT	960
AATTCATTA	AAACCATTAC	CTTAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	1020
AAAAAAAAAA	AAAAAATTCC	TGCGGCCCGC				1049

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAATTCGGCA	CGAGGGGAGA	ATACTTTTTG	CGATGCCTAC	TGGAGACTTT	GATTCGAAGC	60
CCAGTTGGGC	CGACCAGGTG	GAGGAGGAGG	GGGAGGACGA	CAAATGTGTC	ACCAGCGAGC	120
TCCTCAAGGG	GATCCCTCTG	GCCACAGGTG	ACACCAGCCC	AGAGCCAGAG	CTACTGCCGG	180
GAGCTCCACT	GCCGCCTCCC	AAGGAGGTCA	TCAACGGAAA	CATAAAGACA	GTGACAGAGT	240
ACAAGATAGA	TGAGGATGGC	AAGAAGTTCA	AGATTGTCCG	CACCTTCAGG	ATTGAGACCC	300
GGAAGGCTTC	AAAGGCTGTC	GCAAGGAGGA	AGAAGTGAA	GAAGTTCGGG	AACTCAGAGT	360
TTGACCCCCC	CGGACCCAAT	GTGGCCACCA	CCACTGTGTC	TGACGATGTC	TCTATGACGT	420
TCATCACCAG	CAAAGAGGAC	CTGAAGTGCC	AGGAGGAGGA	GGACCCTATG	AACAAATTCA	480
AGGGCCAGAA	GATCGTGTCC	TGCCGCATCT	GCAAGGGCGA	CCACTGGACC	ACCCGCTGCC	540
CCTACAAGGA	TACGCTGGGG	CCCATGCAGA	AGGAGCTGGC	CGAGCAGCTG	GGCCTGTCTA	600
CTGGCGAGAA	GGAGAAGCTG	CCGGGAGAGC	TAGAGCCGGT	GCAGGCCACG	CAGAACAAGA	660
CAGGGAAGTA	TGTGCCGCCG	AGCCTGCGCG	ACGGGGCCAG	CCGCCGCGGG	GAGTCCATGC	720
AGCCCAACCG	CAGAGCCGAC	GACAACGCCA	CCATCCGTGT	CACCAACTTG	CGCAGAGGAC	780
ACGCGTGAGA	CCGACCTGCA	GGAGCTCTTC	CGGCCCTTCG	GCTCCATCTC	CCGCATCTAC	840
CTGGCTAAGG	ACAAGACCAC	TGGCCAATCC	AAGGGCTTTG	CCTTCATCAG	CTTCCACCGC	900

CGCGAGGATG	CTGCGCGTGC	CATTGCCGGG	GTGTCCGGCT	TTGGCTACGA	CCACCTCATC	960
CTCAACGTCG	AGTGGGCCAA	GCCGTCCACC	AACTAAGCCA	GCTGCCACTG	TGTACTCGGT	1020
CCGGGACCCT	TGGCGACAGA	AGACAGCCTC	CGAGAGCGCG	GGCTCCAAGG	GCAATAAAGC	1080
AGCTCCACTC	TCAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAT	TCCTGCGGCC	1140
GC						1142

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1696 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAATTCGGCA	CGAGGGAAAC	ATGGCGGTAG	GCTGGGACCA	TAACACAAGC	ATGACTATAT	60
GAAGGAAGAG	GAAGGTTTT	CTGAAGATGA	GGCGACTGAA	TCGGAAAAAA	ACTTTAAGTT	120
TGGTAAAAGA	GTTGGATGCC	TTTCCGAAGG	TTCTTGAGAG	CTATGTAGAG	ACTTCAGCCA	180
GTGGAGGTAC	AGTTTCTCTA	ATAGCATTTA	CAACTATGGC	TTTATTAACC	ATAATGGAAT	240
TCTCAGTATA	TCAAGATACA	TGGATGAAGT	ATGAATACGA	AGTAGACAAG	GATTTTTCTA	300
GCAAATTAAG	AATTAATATA	GATATTACTG	TTGCCATGAA	GTGTCAATAT	GTTGGAGCGG	360
ATGTATTGGA	TTTAGCAGAA	ACAATGGTTG	CATCTGCAGA	TGGTTTAGTT	TATGAACCAA	420
CAGTATTTGA	TCTTTCACCA	CAGCAGAAA	AGTGGCAGAG	GATGCTGCAG	CTGATTCAGA	480
GTAGGCTACA	AGAAGAGCAT	TCACCTCAAG	ATGTGATATT	TAAAAGTGCT	TTTAAAAGTA	540
CATCAACAGC	TCTTCCACCA	AGAGAAGATG	ATTCATCACA	GTCTCCAAAT	GCATGCAGAA	600
TTCATGGCCA	TCTATATGTC	AATAAAGTAG	CAGGGAATTT	TCACATAACA	GTGGGCAAGG	660
CAATTCCACA	TCCTCGTGGT	CATGCACATT	TGGCAGCACT	TGTCAACCAT	GAATCTTACA	720
ATTTTTCTCA	TAGAATAGAT	CATTTGTCTT	TTGGAGAGCT	TGTTCCAGCA	ATTATTAATC	780
CTTTAGATTG	AACTGAAAA	ATTGCTATAG	ATCACACCA	GATGTTCCAA	TATTTTATTA	840
CAGTTGTGCC	AACAAAACCTA	CATACATATA	AAATATCAGC	AGACACCCAT	CAGTTTTCTG	900
TGACAGAAAG	GGAACGTATC	ATTAACCATG	CTGCAGGCAG	CCATGGAGTC	TCTGGGATAT	960
TTATGAAATA	TGATCTCAGT	TCTCTTATGG	TGACAGTTAC	TGAGGAGCAC	ATGCCATTCT	1020
GGCAGTTTTT	TGTAAGACTC	TGTGGTATTG	TTGGAGGAAT	CTTTTCAACA	ACAGGCATGT	1080
TACATGGAAT	TGGAATAATT	ATAGTTGAAA	TAATTTGCTG	TCGTTTCAGA	CTTGGATCCT	1140
ATAAACCTGT	CAATTCTGTT	CCTTTTGAGG	ATGGCCACAC	AGACAACCAC	TTACCTCTTT	1200
TAGAAAATAA	TACACATTAA	CACCTCCCGA	TTGAAGGAGA	AAAACCTTTT	GCCTGAGACA	1260
TAAAACCTTT	TTTTAATAAT	AAAATATTGT	GCAATATATT	CAAAGAAAAG	AAAACACAAA	1320
TAAGCAGAAA	ACATACTTAT	TTTAAAAAAG	AAAAAAAAGG	ATAAAAAAAC	CCAAACTGAA	1380
ATTCTATATA	CGTTGTGTCT	GTTACAAATG	TCGTAGAAGA	AATCATGCAG	CTAAACGATG	1440
AAGAAGCCCA	ACTGGAGTGT	TGCTTTGAAG	ATGACGCCCT	CTTATATTTT	CATAGCAAAT	1500
GGGTGGTATC	AAAATCAGAC	ATTGCTTCTT	GCTGATAAAA	AGCCTGAAGG	AAATAAGTGA	1560
AACTACATCT	ATGGGAAAA	AAAAAACATT	GAGAAGTGCA	AATGTTTCGA	TCCTTTTGTT	1620
TTTAAAAGAT	ATGATGTCAG	AATAAAATGT	GGAAAACATA	CGGAAAAAAA	AAAAAAAATA	1680
AAATTCCTGC	GGCCGC					1696

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAATTCGGCA	CGAGGCGGCA	CGAGGCGGCA	CGAGGGTGGC	ATATCACGGC	CATGGGGTCT	60
CAGCATTCCG	CTGCTGCTCG	CCCCTCCTCC	TGCAGGCGAA	AGCAAGAAGA	TGACAGGGAC	120
GGTTTGCTGG	CTGAACGAGA	GCAGGAAGAA	GCCATTGCTC	AGTTCCCATA	TGTGGAATTC	180
ACCGGGAGAG	ATAGCATCAC	CTGTCTCACG	TGCCAGGGGA	CAGGCTACAT	TCCAACAGAG	240
CAAGTAAATG	AGTTGGTGGC	TTTGATCCCA	CACAGTGATC	AGAGATTGCG	CCCTCAGCGA	300
ACTAAGCAAT	ATGTCCTCCT	GTCCATCCTG	CTTTGTCTCC	TGGCATCTGG	TTTGGTGGTT	360
TTCTTCCTGT	TTCCGCATTC	AGTCCTTGTC	GATGATGACG	GCATCAAAGT	GGTGAAAGTC	420
ACATTTAATA	AGCAAGACTC	CCTTGTAATT	CTCACCATCA	TGGCCACCCT	GAAAATCAGG	480
AACTCCAAC	TCTACACGGT	GGCAGTGACC	AGCCTGTCCA	GCCAGATTCA	GTACATGAAC	540
ACAGTGGTCA	GTACATATGT	GACTACTAAC	GTCTCCCTTA	TTCCACCTCG	GAGTGAGCAA	600
CTGGTGAATT	TTACCGGGAA	GGCCGAGATG	GGAGGACCGT	TTTCCTATGT	GTAATTCTTC	660
TGCACGGTAC	CTGAGATCCT	GGTGACAAAC	ATAGTGATCT	TCATGCGAAC	TTCAGTGAAG	720
ATTTCATACA	TTGGCCTCAT	GACCCAGAGC	TCCTTGGAGA	CACATCACTA	TGTGGATTGT	780
GGAGGAAATT	CCACAGCTAT	TTAACAAC	CTATTGGTTC	TTCCACACAG	CGCCTGTAGA	840
AGAGAGCACA	GCATATGTTT	CCAAGGCC	AGTTCTGGAC	CTACCCCCAC	GTGGTGTAAG	900
CAGAGGAGGA	ATTGGTTTAC	TTAACTCCCA	GCAAACATCC	TCCTGCCACT	TAGGAGGAAA	960
CACCTCCCTA	TGGTACCATT	TATGTTTCTC	AGAACCAGCA	GAATCAGTGC	CTAGCCTGTG	1020
CCCAGCAAAT	AGTTGGCACT	CAATAAAGAT	TTGCAGAATT	TAAAAAAAAA	AAAAAAAAAA	1080
AAAAAAATTC	CTGCGGCCGC					1100

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAATTCGGCA	CGAGGGTACC	TGCTTTTCTA	TTGCCTCTTT	GAAACAATGG	TCACGTGTTT	60
CCATGTTCCC	TACTCGGCTC	TCACCATGTT	CATCAGCACC	GAGCAGACTG	AGCGGGATTC	120
TGCCACCGCC	TATCGGATGA	CTGTGGAAGT	GCTGGGCACA	GTGCTGGGCA	CGGCGATCCA	180
GGGACAAATC	GTGGGCCAAG	CAGACACGCC	TTGTTTCCAG	GACCTCAATA	GCTCTACAGT	240
AGCTTCACAA	AGTGCCAACC	ATACACATGG	CACCACCTCA	CACAGGGAAA	CGCAAAAGGC	300
ATACCTGCTG	GCAGCGGGGG	TCATTGTCTG	TATCTATATA	ATCTGTGCTG	TCATCCTGAT	360
CCTGGGCGTG	CGGGAGCAGA	GAGAACCCTA	TGAAGCCAG	CAGTCTGAGC	CAATCGCCTA	420
CTTCCGGGGC	CTACGGCTGG	TCATGAGCCA	CGGCCCATAC	ATCAAACCTTA	TTACTGGCTT	480
CCTCTTCACC	TCCTTGGCTT	TCATGCTGGT	GGAGGGGAAC	TTTGTCTTGT	TTTGCACCTA	540
CACCTTGGGC	TTCCGCAATG	AATTCCAGAA	TCTACTCCTG	GCCATCATGC	TCTCGGCCAC	600
TTTAACCATT	CCCATCTGGC	AGTGTTTCTT	GACCCGGTTT	GGCAAGAAGA	CAGCTGTATA	660
TGTTGGGATC	TCATCAGCAG	TGCCATTTCT	CATCTTGGTG	GCCCTCATGG	AGAGTAACCT	720
CATCATTACA	TATGCGGTAG	CTGTGGCAGC	TGGCATCAGT	GTGGCAGCTG	CCTTCTTACT	780
ACCCTGGTCC	ATGCTGCCTG	ATGTCATTGA	CGACTTCCAT	CTGAAGCAGC	CCCACTTCCA	840
TGGAACCGAG	CCCATTCTCT	TCTCCTTCTA	TGTCTTCTTC	ACCAAGTTTG	CCTCTGGAGT	900
GTCACCTGGG	ATTCTTACCC	TCAGTCTGGA	CTTTGCAGGG	TACCAGACCC	GTGGCTGCTC	960
GCAGCCGGAA	CGTGCTCAAGT	TTACACTGAA	CATGCTCGTG	ACCATGGCTC	CCATAGTTCT	1020
CATCCTGCTG	GGCCTGCTGC	TCTTCAAAAT	GTACCCCAT	GATGAGGAGA	GGCGGCGGCA	1080
GAATAAGAAG	GCCCTGCAGG	CACTGAGGGA	CGAGGCCAGC	AGCTCTGGCT	GCTCAGAAAC	1140
AGACTCCACA	GAGCTGGCTA	GCATCCTCTA	GGGCCCGCCA	CGTTGCCCGA	AGCCACCATG	1200
CAGAAGGCCA	CAGAAGGGAT	CAGGACCTGT	CTGCCGGCTT	GCTGAGCAGC	TGGACTGCAG	1260
GTGCTAGGAA	GGGAAGTGA	GACTCAAGGA	GGTGGCCAG	GACACTTGCT	GTGCTCACTG	1320
TGGGGCCGGC	TGCTCTGTGG	CCTCCTGCCT	CCCCTCTGCC	TGCCTGTGGG	GCCAAGCCCT	1380
GGGGCTGCCA	CTGTGAATAT	GCCAAGGACT	GATCGGGCCT	AGCCCGGAAC	ACTAATGTAG	1440
AAACCTTTTT	TTTACAGAGC	CTAATTAATA	ACTTAATGAC	TGTGTACATA	GCAATGTGTG	1500

TGTATGTATA TGTCTGTGAG CTATTAATGT TATTAATTTT CATAAAAGCT GGAAAGCAAA 1560
 AAAAAAAAAA AAAAATTCCT GCGGCCGC 1588

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1535 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAATTCGGCA	CGAGGCGGAA	GTCCCGTCTC	ACGGTTGCCC	TGGCAGCGCG	CGAGGCTGGT	60
GAGTCGGCAG	CCCTGTGGCA	GCCGGCGGGC	TGGTTTCCAT	GGTTGCACGA	TTAGGAACCA	120
CCAGCTGCTG	CATCCCATGG	CCAGGGGTGG	CGTCCAGGTG	GCAGAGCAGC	TAGGAACGCA	180
AGGCCTGAAC	CTGGGGCCAG	ACACCCTGCT	CTCCCGGCCA	TGGTCAACGA	CCCTCCAGTA	240
CCTGCCTTAC	TGTGGGCCCC	GGAGGTGGGC	CAAGTCTTGG	CAGGCCGTGC	CCGCAGGCTG	300
CTGCTGCAGT	TTGGGGTGCT	CTTCTGCACC	ATCCTCCTTT	TGCTCTGGGT	GTCTGTCTTC	360
CTCTATGGCT	CCTTCTACTA	TTCCTATATG	CCGACAGTCA	GCCACCTCAG	CCCTGTGCAT	420
TTCTACTACA	GGACCGACTG	TGATTCCCTC	ACCACCTCAC	TCTGCTCCTT	CCCTGTTGCC	480
AATGTCTCGC	TGACTAAGGG	TGGACGTGAT	CGGGTGCTGA	TGTATGGACA	GCCGTATCGT	540
GTTACCTTAG	AGCTTGAGCT	GCCAGAGTCC	CCTGTGAATC	AAGATTTGGG	CATGTTCTTG	600
GTCACCATTT	CCTGCTACAC	CAGAGGTGGC	CGAATCATCT	CCACTTCTTC	GCGTTCGGTG	660
ATGCTGCATT	ACCGCTCAGA	CCTGCTCCAG	ATGCTGGACA	CACTGGTCTT	CTCTAGCCTC	720
CTGCTATTTG	GCTTTGCAGA	GCAGAAGCAG	CTGCTGGAGG	TGGAACCTA	CGCAGACTAT	780
AGAGAGAACT	CGTACGTGCC	GACCACTGGA	GCGATCATTG	AGATCCACAG	CAAGCGCATC	840
CAGCTGTATG	GAGCCTACCT	CCGCATCCAC	GCGCACTTCA	CTGGGCTCAG	ATACCTGCTA	900
TACAACTTCC	CGATGACCTG	CGCCTTCATA	GGTGTTGCCA	GCAACTTCAC	CTTCCTCAGC	960
GTCATCGTGC	TCTTCAGCTA	CATGCAGTGG	GTGTGGGGGG	GCATCTGGCC	CCGACACCGC	1020
TTCTCTTTGC	AGGTTAACAT	CCGAAAAAGA	GACAATTCCC	GGAAGGAAGT	CCAACGAAGG	1080
ATCTCTGCTC	ATCAGCCAGG	GCCTGAAGGC	CAGGAGGAGT	CAACTCCGCA	ATCAGATGTT	1140
ACAGAGGATG	GTGAGAGCCC	TGAAGATCCC	TCAGGGACAG	AGGTCAGCTG	TCCGAGGAGG	1200
AGAAACCAGA	TCAGCAGCCC	CTGAGCGGAG	AAGAGGAGCT	AGAGCCTGAG	GCCAGTGATG	1260
GTTCAGGCTC	CTGGGAAGAT	GCAGCTTTGC	TGACGGAGGC	CAACCTGCCT	GCTCCTGCTC	1320
CTGCTTCTGC	TTCTGCCCCCT	GTCCTAGAGA	CTCTGGGCAG	CTCTGAACCT	GCTGGGGGTG	1380
CTCTCCGACA	GCGCCCCACC	TGCTCTAGTT	CCTGAAGAAA	AGGGGCAGAC	TCCTCACATT	1440
CCAGCACTTT	CCCACCTGAC	TCCTCTCCCC	TCGTTTTTTC	TTCAATAAAC	TATTTTGTGT	1500
CAAAAAAAAA	AAAAAAAAAA	AATTCCTGCG	GCCGC			1535

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAATTCGGCA	CGAGGGCGGG	CGCTACGGGC	TTGACTCCCC	CAAGGCCGAG	GTCCGCGGCC	60
AGGTGCTGGC	GCCGCTGCCC	CTCCACGGAG	TTGCTGATCA	TCTGGGCTGT	GATCCACAAA	120
CCCGGTTCTT	TGTCCCTCCT	AATATCAAAC	AGTGGATTGC	CTTGCTGCAG	AGGGGAAACT	180
GCACGTTTAA	AGAGAAAATA	TCACGGGCCG	CTTTCCACAA	TGCAGTTGCT	GTAGTCATCT	240
ACAATAATAA	ATCCAAAGAG	GAGCCAGTTA	CCATGACTCA	TCCAGGCACT	GGAGATATTA	300

TTGCTGTCAT	GATAACAGAA	TTGAGGGGTA	AGGATATTTT	GAGTTATCTG	GAGAAAAACA	360
TCTCTGTACA	AATGACAATA	GCTGTTGGAA	CTCGAATGCC	ACCGAAGAAC	TTCAGCCGTG	420
GCTCTCTAGT	CTTCGTGTCA	ATATCCTTTA	TTGTTTTGAT	GATTATTTCT	TCAGCATGGC	480
TCATATTCTA	CTTCATTCAA	AAGATCAGGT	ACACAAATGC	ACGCGACAGG	AACCAGCGTC	540
GTCTCGGAGA	TGCAGCCAAG	AAAGCCATCA	GTAAATTGAC	AACCAGGACA	GTAAAGAAGG	600
GTGACAAGGA	AACTGACCCA	GACTTTGATC	ATTGTGCAGT	CTGCATAGAG	AGCTATAAGC	660
AGAATGATGT	CGTCCGAATT	CTCCCCTGCA	AGCATGTTTT	CCACAAATCC	TGCGTGGATC	720
CCTGGCTTAG	TGAACATTGT	ACCTGTCCTA	TGTGCAAACT	TAATATATTG	AAGGCCCTGG	780
GAATTGTGCC	GAATTTGCCA	TGTACTGATA	ACGTAGCATT	CGATATGGAA	AGGCTCACCA	840
GAACCAAGC	TGTTAACC GA	AGATCAGCCC	TCGGCGACCT	CGCCGGCGAC	AACTCCCTTG	900
GCCTTGAGCC	ACTTCGAACT	TCGGGGATCT	CACCTCTTCC	TCAGGATGGG	GAGCTCACTC	960
CGAGAACAGG	AGAAATCAAC	ATTGCAGTAA	CAAAAGAATG	GTTTATTATT	GCCAGTTTTG	1020
GCCTCCTCAG	TGCCCTCACA	CTCTGCTACA	TGATCATCAG	AGCCACAGCT	AGCTTGAATG	1080
CTAATGAGGT	AGAATGTTTT	TGAAGAAGAA	AAAACCTGCT	TTCTGACTGA	TTTTGCCTTG	1140
AAGGAAAAAA	GAACCTATTT	TTGTGCATCA	TTTACCAATC	ATGCCACACA	AGCATTTTATT	1200
TTTAGTACAT	TTTATTTTTT	CATAAAATTG	CTAATGCCAA	AGCTTTGTAT	TAAAAGAAAT	1260
AAATAATAAA	ATAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAT	TCCTGCGGCC	1320
GC						1322

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAATTCGGCA	CGAGGCCCTC	CCGCGCTCCC	GGGCGCGCGG	GGCCGCGCCC	CCGACGCCCT	60
ACATATACTC	AGGTGCGCCC	CACCTGTCCG	CCCGCACCTG	CTGGCTCACC	TCCGAGCCAC	120
CTCTGCTGCG	CACCGCAGCC	TCGGACCTAC	AGCCCAGGAT	ACTTTGGGAC	TTGCCGGCGC	180
TCAGAAACGC	GCCCAGACGG	CCCCTCCACC	TTTTGTTTGC	CTAGGGTCGC	CGAGAGCGCC	240
CGGAGGGAAC	CGCCTGGCCT	TCGGGGACCA	CCAATTTTGT	CTGGAACCAC	CCTCCCGGCG	300
TATCCTACTC	CCTGTGCCGC	GAGGCCATCG	CTTCACTGGA	GGGGTCGATT	TGTGTGTAGT	360
TTGGTGACAA	GATTTGCATT	CACCTGGCCC	AAACCCTTTT	TGTCTCTTTG	GGTGACCGGA	420
AAACTCCACC	TCAAGTTTTT	TTTTGTGGGG	CTGCCCCCA	AGTGTCTGTT	GTTTTACTGT	480
AGGGTCTCCC	GCCCGGCGCC	CCCAGTGTTT	TCTGAGGGCG	GAAATGGCCA	ATTCGGGCCT	540
GCAGTTGCTG	GGCTTCTCCA	TGGCCCTGCT	GGGCTGGGTG	GGTCTGGTGG	CCTGCACCGC	600
CATCCCGCAG	TGGCAGATGA	GCTCCTATGC	GGGTGACAAC	ATCATCACGG	CCCAGGCCAT	660
GTACAAGGGG	CTGTGGATGG	ACTGCGTCAC	GCAGAGCACG	GGGATGATGA	GCTGCAAAAT	720
GTACGACTCG	GTGCTCGCCC	TGTCCGCGGC	CTTGCAGGCC	ACTCGAGCCC	TAATGGTGGT	780
CTCCCTGGTG	CTGGGCTTCC	TGGCCATGTT	TGTGGCCACG	ATGGGCATGA	AGTGCACGCG	840
CTGTGGGGGA	GACGACAAAG	TGAAGAAGGC	CCGTATAGCC	ATGGGTGGAG	GCATAATTTT	900
CATCGTGGCA	GGTCTTGCCG	CCTTGGTAGC	TTGCTCCTGG	TATGGCCATC	AGATTGTCAC	960
AGACTTTTAT	AACCCTTTGA	TCCCTACCAA	CATTAAGTAT	GAGTTTGGCC	CTGCCATCTT	1020
TATTGGCTGG	GCAGGGTCTG	CCCTAGTCAT	CCTGGGAGGT	GCATGCTCT	CCTGTTCTCTG	1080
TCCTGGGAAT	GAGAGCAAGG	CTGGGTACCG	TGCACCCCGC	TCTTACCCTA	AGTCCAACCTC	1140
TTCCAAGGAG	TATGTGTGAC	CTGGGATCTC	CTTGCCCCAG	CCTGACAGGC	TATGGGAGTG	1200
TCTAGATGCC	TGAAAGGGCC	TGGGGCTGAG	CTCAGCCTGT	GGGCAGGGTG	CCGGACAAAG	1260
GCCTCCTGGT	CACTCTGTCC	CTGCACTCCA	TGTATAGTCC	TCTTGGGTTG	GGGGTGGGGG	1320
GGTGCCGTTG	GTGGGAGAGA	CAAAAAGAGG	GAGAGTGTGC	TTTTTTGTACA	GTAATAAAAA	1380
ATAAGTATTG	GGAAGCAGGC	TTTTTTCCCT	TCAGGGCCTC	TGCTTTCCCTC	CCGTCCAGAT	1440
CCTTGACAGG	AGCTTGGAAC	CTTAGTGCAC	CTACTTCAGT	TCAGAACACT	TAGCACCCCA	1500
CTGACTCCAC	TGACAATTGA	CTAAAAGATG	CAGGTGCTCG	TATCTCGACA	TTCAATCCCA	1560
CCCCCTCTT	ATTAAATAG	CTACCAAAGT	ACTTCTTTTT	TAATAAAAAA	ATAAAGATTT	1620

TTATTAGGTA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1680
 AAAAAAAAAA AAAAAAATT CCTGCGGCCG C 1711

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1553 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAATTCGGCA	CGAGGGCAGG	TCCAGAGTAA	AGTCACTGAA	GAGTGAAGC	GAGGAAGGAA	60
CAGGATGATT	AGACCTCAGC	TGCGGACCGC	GGGGCTGGGA	CGATGCCTCC	TGCCGGGGCT	120
GCTGCTGCTC	CTGGTGCCCG	TCCTCTGGGC	CGGGGCTGAA	AAGCTACATA	CCCAGCCCTC	180
CTGCCCCGCG	GTCTGCCAGC	CCACGCGCTG	CCCCGCGCTG	CCCACCTGCG	CGCTGGGGAC	240
CACGCCGGTG	TTCGACCTGT	GCCGCTGTTG	CCGCGTCTGC	CCCGCGGCCG	AGCGTGAAGT	300
CTGCGGCGGG	GCGCAGGGCC	AACCGTGCGC	CCCGGGGCTG	CAGTGCCTCC	AGCCGCTGCG	360
CCCCGGGTTC	CCCAGCACCT	GCGGTTGCCC	GACGCTGGGA	GGGGCCGTGT	GCGGCAGCGA	420
CAGGCGCACC	TACCCAGCA	TGTGCGCGCT	CCGGGCCGAA	AACCGCGCCG	CGCGCCGCCT	480
GGGCAAGGTC	CCGGCCGTGC	CTGTGCAGTG	GGGGAAGTGC	GGGGATACAG	GGACCAGAAG	540
CGCAGGCCCG	CTCAGGAGGA	ATTACAACCT	CATCGCCGCG	GTGGTGGAGA	AGGTGGCGCC	600
ATCGGTGGTT	CACGTGCAGC	TGTGGGGCAG	GTTACTTCAC	GGCAGCAGGC	TTGTTCTCTGT	660
GTACAGTGGC	TCTGGGTTC	TAGTGTCTGA	GGACGGGCTC	ATTATTACCA	ATGCCCATGT	720
TGTCAGGAAC	CAGCAGTGA	TTGAGGTGGT	GCTCCAGAAT	GGGGCCCGTT	ATGAAGCTGT	780
TGTCAAGGAT	ATTGACCTTA	AATTGGATCT	TGCGGTGATT	AAGATTGAAT	CAAATGCTGA	840
ACTTCCTGTA	CTGATGCTGG	GAAGATCATC	TGACCTTCGG	GCTGGAGAGT	TTGTGGTGCC	900
TTTGGGCAGC	CCATTTTCTC	TGCAGAACAC	AGCTACTGCA	GGAATTGTCA	GCACCAACA	960
GCGAGGGGGC	AAAGAACTGG	GGATGAAGGA	TTCAGATATG	GACTACGTCC	AGATTGATGC	1020
CACAATTAAC	TATGGGAATT	CTGGTGGTCC	TCTGGTGAAC	TTGGATGGTG	ATGTGATTGG	1080
CGTCAATTCA	TTGAGGTGA	CTGATGGAAT	CTCCTTTGCA	ATTCCTTCAG	ATCGAGTTAG	1140
GCAGTTCTTG	GCAGAATACC	ATGAGCACCA	GATGAAAGGA	AAGGCGTTTT	CAAATAAGAA	1200
ATATCTGGGT	CTGCAATGC	TGTCCCTCAC	TGTGCCCTTT	AGTGAAGAAT	TGAAAATGCA	1260
TTATCCAGAT	TTCCCTGATG	TGAGTTCTGG	GGTTTATGTA	TGTAAAGTGG	TTGAAGGAAC	1320
AGCTGCTCAA	AGCTCTGGAT	TGAGAGATCA	CGATGTAATT	GTCAACATAA	ATGGGAAACC	1380
TATTACTACT	ACAACCTGATG	TTGTTAAAGC	TCTTGACAGT	GATTCCCTTT	CCATGGCTGT	1440
TCTTCGGGGA	AAAGATAATT	TGCTCCTGAC	AGTCATACCT	GAAACAATCA	ATTAAATATC	1500
TTGTTTTAAA	GTGGGATTAT	CTAAAAAAA	AAAAAAA	TTCCTGCGGC	CGC	1553

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1596 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAATTCGGCA	CGAGGGGAGC	CGCTCCCGGA	GCCCGGCCGT	AGAGGCTGCA	ATCGCAGCCG	60
GGAGCCCGCA	GCCCGCGCCC	CGAGCCCGCC	GCCGCCCTTC	GAGGGCGCCC	CAGGCCGCGC	120
CATGGTGAAG	GTGACGTTCA	ACTCCGCTCT	GGCCCAAGAG	GAGGCCAAGA	AGGACGAGCC	180
CGAGAGCGGC	GAGGAGGCGC	TCATCATCCC	CCCCGACGCC	GTCGCGGTGG	ACTGCAAGGA	240

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CCCAGATGAT GTGGTACCAG TTGGCCAAAG AAGAGCCTGG TGTGCTTTGG 300
ACTAGCATT ATGCTTGCAG GTGTTATTCT AGGAGGAGCA TACTTGTACA AATATTTTGC 360
ACTTCAACCA GATGACGTGT ACTACTGTGG AATAAAGTAC ATCAAAGATG ATGTCATCTT 420
AAATGAGCCC TCTGCAGATG CCCCAGCTGC TCTCTACCAG ACAATTGAAG AAAATATTAA 480
AATCTTTGAA GAAGAAGAAG TTGAATTTAT CAGTGTGCCT GTCCCAGAGT TTGCAGATAG 540
TGATCCTGCC AACATTGTTC ATGACTTTAA CAAGAACTT ACAGCCTATT TAGATCTTAA 600
CCTGGATAAG TGCTATGTGA TCCCTCTGAA CACTTCCATT GTTATGCCAC CCAGAAACCT 660
ACTGGAGTTA CTTATTAACA TCAAGGCTGG AACCTATTTG CCTCAGTCCT ATCTGATTCA 720
TGAGCACATG GTTATTACTG ATCGCATTGA AAACATTGAT CACCTGGGTT TCTTTATTTA 780
TCGACTGTGT CATGACAAGG AAACCTACAA ACTGCAACGC AGAGAAACTA TTAAAGGTAT 840
TCAGAAACGT GAAGCCAGCA ATTGTTTCGC AATTCGGCAT TTTGAAAACA AATTTGCCGT 900
GGAAACTTTA ATTTGTTCTT GAACAGTCAA GAAAAACATT ATTGAGGAAA ATTAATATCA 960
CAGCATAACC CCACCCTTTA CATTTTGTGC AGTGATATTT TTTAAAGTCT CTTTCATGTA 1020
AGTAGCAAAC AGGGCTTTAC TATCTTTTCA TCTCATTAAT TCAATTAAAA CCATTACCTT 1080
AAAATTTTTT TCTTTCGAAG TGTGGTGTCT TTTATATTTG AATTAGTAAC TGTATGAAGT 1140
CATAGATAAT AGTACATGTC ACCTTAGGTA GTAGGAAGAA TTACAATTTT TTTAAATCAT 1200
TTATCTGGAT TTTTATGTTT TATTAGCATT TTCAAGAAGA CGGATTATCT AGAGAATAAT 1260
CATATATATG CATACGTAAA AATGGACCAC AGTGACTTAT TTGTAGTTGT TAGTTGCCCT 1320
GCTACCTAGT TTGTTAGTGC ATTTGAGCAC ACATTTTAAT TTTCTCTAA TTTAAATGTG 1380
CAGTATTTTC AGTGTCAAAT ATATTTAACT ATTTAGAGAA TGATTTCCAC CTTTATGTTT 1440
TAATATCCTA GGCATCTGCT GTAATAATAT TTTAGAAAAT GTTTGGAATT TAAGAAATAA 1500
CTTGTGTTAC TAATTTGTAT AACCCATATC TGTGCAATGG AATATAAATA TCACAAAGTT 1560
GTTTAAAAAA AAAAAAATAA AAATTCCTGC GGCCGC 1596

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(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

Met Ala Trp Arg Arg Arg Glu Ala Gly Val Gly Ala Arg Gly Val Leu
 1           5           10           15
Ala Leu Ala Leu Leu Ala Leu Ala Leu Cys Val Pro Gly Ala Arg Gly
 20           25           30
Arg Ala Leu Glu Trp Phe Ser Ala Val Val Asn Ile Glu Tyr Val Asp
 35           40           45
Pro Gln Thr Asn Leu Thr Val Trp Ser Val Ser Glu Ser Gly Arg Phe
 50           55           60
Gly Asp Ser Ser Pro Lys Glu Gly Ala His Gly Leu Val Gly Val Pro
 65           70           75           80
Trp Ala Pro Gly Gly Asp Leu Glu Gly Cys Ala Pro Asp Thr Arg Phe
 85           90           95
Phe Val Pro Glu Pro Gly Gly Arg Gly Ala Ala Pro Trp Val Ala Leu
 100          105          110
Val Ala Arg Gly Gly Cys Thr Phe Lys Asp Lys Val Leu Val Ala Ala
 115          120          125
Arg Arg Asn Ala Ser Ala Val Val Leu Tyr Asn Glu Glu Arg Tyr Gly
 130          135          140
Asn Ile Thr Leu Pro Met Ser His Ala Gly Thr Gly Asn Ile Val Val
 145          150          155          160
Ile Met Ile Ser Tyr Pro Lys Gly Arg Glu Ile Leu Glu Leu Val Gln

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115	120	125
Pro Asn Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser		
130	135	140
Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg		
145	150	155
Leu Phe Leu Asn Trp Thr Glu Gly Gln Glu Ser Gly Phe Leu Arg Ile		160
	165	170
Ser Asn Leu Arg Lys Glu Asp Gln Ser Val Tyr Phe Cys Arg Val Glu		175
	180	185
Leu Asp Thr Arg Arg Ser Gly Arg Gln Gln Leu Gln Ser Ile Lys Gly		190
	195	200
Thr Lys Leu Thr Ile Thr Gln Ala Val Thr Thr Thr Thr Thr Trp Arg		205
	210	215
Pro Ser Ser Thr Thr Thr Ile Ala Gly Leu Arg Val Thr Glu Ser Lys		220
225	230	235
Gly His Ser Glu Ser Trp His Leu Ser Leu Asp Thr Ala Ile Arg Val		240
	245	250
Ala Leu Ala Val Ala Val Leu Lys Thr Val Ile Leu Gly Leu Leu Cys		255
	260	265
Leu Leu Leu Leu Trp Trp Arg Arg Arg Lys Gly Ser Arg Ala Pro Ser		270
	275	280
Ser Asp Phe		285
290		

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met	Thr	Val	Ser	Gln	Arg	Phe	Gln	Leu	Ser	Asn	Ser	Gly	Pro	Asn	Ser
1				5				10						15	
Thr	Ile	Lys	Met	Lys	Ile	Ala	Leu	Arg	Val	Leu	His	Leu	Glu	Lys	Arg
		20					25						30		
Glu	Arg	Pro	Pro	Asp	His	Gln	His	Ser	Ala	Gln	Val	Lys	Arg	Pro	Ser
		35				40						45			
Val	Ser	Lys	Glu	Gly	Arg	Lys	Thr	Ser	Ile	Lys	Ser	His	Met	Ser	Gly
	50				55					60					
Ser	Pro	Gly	Pro	Gly	Gly	Ser	Asn	Thr	Ala	Pro	Ser	Thr	Pro	Val	Ile
65				70					75					80	
Gly	Gly	Ser	Asp	Lys	Pro	Gly	Met	Glu	Glu	Lys	Ala	Gln	Pro	Pro	Glu
			85				90					95			
Ala	Gly	Pro	Gln	Gly	Leu	His	Asp	Leu	Gly	Arg	Ser	Ser	Ser	Ser	Leu
		100					105					110			
Leu	Ala	Ser	Pro	Gly	His	Ile	Ser	Val	Lys	Glu	Pro	Thr	Pro	Ser	Ile
		115				120						125			
Ala	Ser	Asp	Ile	Ser	Leu	Pro	Ile	Ala	Thr	Gln	Glu	Leu	Arg	Gln	Arg
	130					135				140					
Leu	Arg	Gln	Leu	Glu	Asn	Gly	Thr	Thr	Leu	Gly	Gln	Ser	Pro	Leu	Gly
145				150					155					160	
Gln	Ile	Gln	Leu	Thr	Ile	Arg	His	Ser	Ser	Gln	Arg	Asn	Lys	Leu	Ile

				165					170					175			
Val	Val	Val	His	Ala	Cys	Arg	Asn	Leu	Ile	Ala	Phe	Ser	Glu	Asp	Gly		
			180					185					190				
Ser	Asp	Pro	Tyr	Val	Arg	Met	Tyr	Leu	Leu	Pro	Asp	Lys	Arg	Arg	Ser		
		195					200					205					
Gly	Arg	Arg	Lys	Thr	His	Val	Ser	Lys	Lys	Thr	Leu	Asn	Pro	Val	Phe		
	210				215						220						
Asp	Gln	Ser	Phe	Asp	Phe	Ser	Val	Ser	Leu	Pro	Glu	Val	Gln	Arg	Arg		
	225				230					235					240		
Thr	Leu	Asp	Val	Ala	Val	Lys	Asn	Ser	Gly	Gly	Phe	Leu	Ser	Lys	Asp		
			245						250					255			
Lys	Gly	Leu	Leu	Gly	Lys	Val	Leu	Val	Ala	Leu	Ala	Ser	Glu	Glu	Leu		
		260					265						270				
Ala	Lys	Gly	Trp	Thr	Gln	Trp	Tyr	Asp	Leu	Thr	Glu	Asp	Gly	Thr	Arg		
	275						280					285					
Pro	Gln	Ala	Met	Thr													
	290																

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met	Glu	Arg	Arg	His	Pro	Val	Cys	Ser	Gly	Thr	Cys	Gln	Pro	Thr	Gln		
1				5					10					15			
Phe	Arg	Cys	Ser	Asn	Gly	Cys	Cys	Ile	Asp	Ser	Phe	Leu	Glu	Cys	Asp		
		20						25				30					
Asp	Thr	Pro	Asn	Cys	Pro	Asp	Ala	Ser	Asp	Glu	Ala	Ala	Cys	Glu	Lys		
	35					40					45						
Tyr	Thr	Ser	Gly	Phe	Asp	Glu	Leu	Gln	Arg	Ile	His	Phe	Pro	Ser	Asp		
	50				55					60							
Lys	Gly	His	Cys	Val	Asp	Leu	Pro	Asp	Thr	Gly	Leu	Cys	Lys	Glu	Ser		
	65				70				75					80			
Ile	Pro	Arg	Trp	Tyr	Tyr	Asn	Pro	Phe	Ser	Glu	His	Cys	Ala	Arg	Phe		
		85						90					95				
Thr	Tyr	Gly	Gly	Cys	Tyr	Gly	Asn	Lys	Asn	Asn	Phe	Glu	Glu	Glu	Gln		
		100					105						110				
Gln	Cys	Leu	Glu	Ser	Cys	Arg	Gly	Ile	Ser	Lys	Lys	Asp	Val	Phe	Gly		
	115					120						125					
Leu	Arg	Arg	Glu	Ile	Pro	Ile	Pro	Ser	Thr	Gly	Ser	Val	Glu	Met	Ala		
	130				135					140							
Val	Ala	Val	Phe	Leu	Val	Ile	Cys	Ile	Val	Val	Val	Val	Ala	Ile	Leu		
	145				150				155						160		
Gly	Tyr	Cys	Phe	Phe	Lys	Asn	Gln	Arg	Lys	Asp	Phe	His	Gly	His	His		
		165						170					175				
His	His	Pro	Pro	Pro	Thr	Pro	Ala	Ser	Ser	Thr	Val	Ser	Thr	Thr	Glu		
		180					185					190					
Asp	Thr	Glu	His	Leu	Val	Tyr	Asn	His	Thr	Thr	Arg	Pro	Leu				
	195						200					205					

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```

Met Ala Gly Leu Ser Arg Gly Ser Ala Arg Ala Leu Leu Ala Ala Leu
 1           5           10           15
Leu Ala Ser Thr Leu Leu Ala Leu Leu Val Ser Pro Ala Arg Gly Arg
          20           25           30
Gly Gly Arg Asp His Gly Asp Trp Asp Glu Ala Ser Arg Leu Pro Pro
          35           40           45
Leu Pro Pro Arg Glu Asp Ala Ala Arg Val Ala Arg Phe Val Thr His
          50           55           60
Val Ser Asp Trp Gly Ala Leu Ala Thr Ile Ser Thr Leu Glu Ala Val
65           70           75           80
Arg Gly Arg Pro Phe Ala Asp Val Leu Ser Leu Ser Asp Gly Pro Pro
          85           90           95
Gly Ala Gly Ser Gly Val Pro Tyr Phe Tyr Leu Ser Pro Leu Gln Leu
          100          105          110
Ser Val Ser Asn Leu Gln Glu Asn Pro Tyr Ala Thr Leu Thr Met Thr
          115          120          125
Leu Ala Gln Thr Asn Phe Cys Lys Lys His Gly Phe Asp Pro Gln Ser
          130          135          140
Pro Leu Cys Val His Ile Met Leu Ser Gly Thr Val Thr Lys Val Asn
145          150          155          160
Glu Thr Glu Met Asp Ile Ala Lys His Ser Leu Phe Ile Arg His Pro
          165          170          175
Glu Met Lys Thr Trp Pro Ser Ser His Asn Trp Phe Phe Ala Lys Leu
          180          185          190
Asn Ile Thr Asn Ile Trp Val Leu Asp Tyr Phe Gly Gly Pro Lys Ile
          195          200          205
Val Thr Pro Glu Glu Tyr Tyr Asn Val Thr Val Gln
210          215          220

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(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

Met Asp His His Cys Pro Trp Leu Asn Asn Cys Val Gly His Tyr Asn
 1           5           10           15
His Arg Tyr Phe Phe Ser Phe Cys Phe Phe Met Thr Leu Gly Cys Val
          20           25           30

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Tyr Cys Ser Tyr Gly Ser Trp Asp Leu Phe Arg Glu Ala Tyr Ala Ala
   35                               40                               45
Ile Glu Lys Met Lys Gln Leu Asp Lys Asn Lys Leu Gln Ala Val Ala
   50                               55                               60
Asn Gln Thr Tyr His Gln Thr Pro Pro Pro Thr Phe Ser Phe Arg Glu
  65                               70                               75                               80
Arg Met Thr His Lys Ser Leu Val Tyr Leu Trp Phe Leu Cys Ser Ser
           85                               90                               95
Val Ala Leu Ala Leu Gly Ala Leu Thr Val Trp His Ala Val Leu Ile
           100                               105                               110
Ser Arg Gly Glu Thr Ser Ile Glu Arg His Ile Asn Lys Lys Glu Arg
  115                               120                               125
Arg Arg Leu Gln Ala Lys Gly Arg Val Phe Arg Asn Pro Tyr Asn Tyr
  130                               135                               140
Gly Cys Leu Asp Asn Trp Lys Val Phe Leu Gly Val Asp Thr Gly Arg
  145                               150                               155                               160
His Trp Leu Thr Arg Val Leu Leu Pro Ser Thr His Leu Pro His Gly
           165                               170                               175
Asn Gly Met Ser Trp Glu Pro Pro Pro Trp Val Thr Ala His Ser Ala
           180                               185                               190
Ser Val Met Ala Val
           195

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(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

Met Ala Pro Leu Gly Met Leu Leu Gly Leu Leu Met Ala Ala Cys Phe
  1                               5                               10                               15
Thr Phe Cys Leu Ser His Gln Asn Leu Lys Glu Phe Ala Leu Thr Asn
  20                               25                               30
Pro Glu Lys Ser Ser Thr Lys Glu Thr Glu Arg Lys Glu Thr Lys Ala
  35                               40                               45
Glu Glu Glu Leu Asp Ala Glu Val Leu Glu Val Phe His Pro Thr His
  50                               55                               60
Glu Trp Gln Ala Leu Gln Pro Gly Gln Ala Val Pro Ala Gly Ser His
  65                               70                               75                               80
Val Arg Leu Asn Leu Gln Thr Gly Glu Arg Glu Ala Lys Leu Gln Tyr
           85                               90                               95
Glu Asp Lys Phe Arg Asn Asn Leu Lys Gly Lys Arg Leu Asp Ile Asn
  100                               105                               110
Thr Asn Thr Tyr Thr Ser Gln Asp Leu Lys Ser Ala Leu Ala Lys Phe
  115                               120                               125
Lys Glu Gly Ala Glu Met Glu Ser Ser Lys Glu Asp Lys Ala Arg Gln
  130                               135                               140
Ala Glu Val Lys Arg Leu Phe Arg Pro Ile Glu Glu Leu Lys Lys Asp
  145                               150                               155                               160
Phe Asp Glu Leu Asn Val Val Ile Glu Thr Asp Met Gln Ile Met Val
           165                               170                               175

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Arg Leu Ile Asn Lys Phe Asn Ser Ser Ser Ser Ser Leu Glu Glu Lys
      180                      185                      190
Ile Ala Ala Leu Phe Asp Leu Glu Tyr Tyr Val His Gln Met Asp Asn
      195                      200                      205
Ala Gln Asp Leu Leu Ser Phe Gly Gly Leu Gln Val Val Ile Asn Gly
      210                      215                      220
Leu Asn Ser Thr Glu Pro Leu Val Lys Glu Tyr Ala Ala Phe Val Leu
      225                      230                      235                      240
Gly Ala Ala Phe Ser Ser Asn Pro Lys Val Gln Val Glu Ala Ile Glu
      245                      250                      255
Gly Gly Ala Leu Gln Lys Leu Leu Val Ile Leu Ala Thr Glu Gln Pro
      260                      265                      270
Leu Thr Ala Lys Lys Lys Val Leu Phe Ala Leu Cys Ser Leu Leu Arg
      275                      280                      285
His Phe Pro Tyr Ala Gln Arg Gln Phe Leu Lys Leu Gly Gly Leu Gln
      290                      295                      300
Val Leu Arg Thr Leu Val Gln Glu Lys Gly Thr Glu Val Leu Ala Val
      305                      310                      315                      320
Arg Val Val Thr Leu Leu Tyr Asp Leu Val Thr Glu Lys Met Phe Ala
      325                      330                      335
Glu Glu Glu Ala Glu Leu Thr Gln Glu Met Ser Pro Glu Lys Leu Gln
      340                      345                      350
Gln Tyr Arg Gln Val His Leu Leu Pro Gly Leu Trp Glu Gln Gly Trp
      355                      360                      365
Cys Glu Ile Thr Ala His Leu Leu Ala Leu Pro Glu His Asp Ala Arg
      370                      375                      380
Glu Lys Val Leu Gln Thr Leu Gly Val Leu Leu Thr Thr Cys Arg Asp
      385                      390                      395                      400
Arg Tyr Arg Gln Asp Pro Gln Leu Gly Arg Thr Leu Ala Ser Leu Gln
      405                      410                      415
Ala Glu Tyr Gln Val Leu Ala Ser Leu Glu Leu Gln Asp Gly Glu Asp
      420                      425                      430
Glu Gly Tyr Phe Gln Glu Leu Leu Gly Ser Val Asn Ser Leu Leu Lys
      435                      440                      445
Glu Leu Arg
      450

```

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```

Met Trp Gln Ala Gly Lys Arg Gln Ala Ser Arg Ala Phe Ser Leu Tyr
  1              5              10              15
Ala Asn Ile Asp Ile Leu Arg Pro Tyr Phe Asp Val Glu Pro Ala Gln
      20              25              30
Val Arg Ser Arg Leu Leu Glu Ser Met Ile Pro Ile Lys Met Val Asn
      35              40              45
Phe Pro Gln Lys Ile Ala Gly Glu Leu Tyr Gly Pro Leu Met Leu Val
      50              55              60

```

```

Phe Thr Leu Val Ala Ile Leu Leu His Gly Met Lys Thr Ser Asp Thr
65          70          75          80
Ile Ile Arg Glu Gly Thr Leu Met Gly Thr Ala Ile Gly Thr Cys Phe
          85          90          95
Gly Tyr Trp Leu Gly Val Ser Ser Phe Ile Tyr Phe Leu Ala Tyr Leu
          100         105         110
Cys Asn Ala Gln Ile Thr Met Leu Gln Met Leu Ala Leu Leu Gly Tyr
          115         120         125
Gly Leu Phe Gly His Cys Ile Val Leu Phe Ile Thr Tyr Asn Ile His
          130         135         140
Leu His Ala Leu Phe Tyr Leu Phe Trp Leu Leu Val Gly Gly Leu Ser
145          150         155         160
Thr Leu Arg Met Val Ala Val Leu Val Ser Arg Thr Val Gly Pro Thr
          165         170         175
Gln Arg Leu Leu Leu Cys Gly Thr Leu Ala Ala Leu His Met Leu Phe
          180         185         190
Leu Leu Tyr Leu His Phe Ala Tyr His Lys Val Val Glu Gly Ile Leu
          195         200         205
Asp Thr Leu Glu Gly Pro Asn Ile Pro Pro Ile Gln Arg Val Pro Arg
          210         215         220
Asp Ile Pro Ala Met Leu Pro Ala Ala Arg Leu Pro Thr Thr Val Leu
225          230         235         240
Asn Ala Thr Ala Lys Ala Val Ala Val Thr Leu Gln Ser His
          245         250

```

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```

Met Gly Ser Glu Asn Glu Ala Leu Asp Leu Ser Met Lys Ser Val Pro
1          5          10          15
Trp Leu Lys Ala Gly Glu Val Ser Pro Pro Ile Phe Gln Glu Asp Ala
          20          25          30
Ala Leu Asp Leu Ser Val Ala Ala His Arg Lys Ser Glu Pro Pro Pro
          35          40          45
Glu Thr Leu Tyr Asp Ser Gly Ala Ser Val Asp Ser Ser Gly His Thr
          50          55          60
Val Met Glu Lys Leu Pro Ser Gly Met Glu Ile Ser Phe Ala Pro Ala
65          70          75          80
Thr Ser His Glu Ala Pro Ala Met Met Asp Ser His Ile Ser Ser Ser
          85          90          95
Asp Ala Ala Thr Glu Met Leu Ser Gln Pro Asn His Pro Ser Gly Glu
          100         105         110
Val Lys Ala Glu Asn Asn Ile Glu Met Val Gly Glu Ser Gln Ala Ala
          115         120         125
Lys Val Ile Val Ser Val Glu Asp Ala Val Pro Thr Ile Phe Cys Gly
          130         135         140
Lys Ile Lys Gly Leu Ser Gly Val Ser Thr Lys Asn Phe Ser Phe Lys
145          150         155         160

```

Arg	Glu	Asp	Ser	Val	Leu	Gln	Gly	Tyr	Asp	Ile	Asn	Ser	Gln	Gly	Glu
				165					170					175	
Glu	Ser	Met	Gly	Asn	Ala	Glu	Pro	Leu	Arg	Lys	Pro	Ile	Lys	Asn	Arg
			180					185					190		
Ser	Ile	Lys	Leu	Lys	Lys	Val	Asn	Ser	Gln	Glu	Val	His	Met	Leu	Pro
		195					200					205			
Ile	Lys	Lys	Gln	Arg	Leu	Ala	Thr	Phe	Phe	Pro	Arg	Lys			
	210					215					220				

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met	Val	Lys	Val	Thr	Phe	Asn	Ser	Ala	Leu	Ala	Gln	Lys	Glu	Ala	Lys
1				5					10					15	
Lys	Asp	Glu	Pro	Lys	Ser	Gly	Glu	Glu	Ala	Leu	Ile	Ile	Pro	Pro	Asp
			20					25					30		
Ala	Val	Ala	Val	Asp	Cys	Lys	Asp	Pro	Asp	Asp	Val	Val	Pro	Val	Gly
		35				40					45				
Gln	Arg	Arg	Ala	Trp	Cys	Trp	Cys	Met	Cys	Phe	Gly	Leu	Ala	Phe	Met
	50				55					60					
Leu	Ala	Gly	Val	Ile	Leu	Gly	Gly	Ala	Tyr	Leu	Tyr	Lys	Tyr	Phe	Ala
	65			70					75					80	
Leu	Gln	Pro	Asp	Asp	Val	Tyr	Tyr	Cys	Gly	Ile	Lys	Tyr	Ile	Lys	Asp
			85					90					95		
Asp	Val	Ile	Leu	Asn	Glu	Pro	Ser	Ala	Asp	Ala	Pro	Ala	Ala	Leu	Tyr
			100					105					110		
Gln	Thr	Ile	Glu	Glu	Asn	Ile	Lys	Ile	Phe	Glu	Glu	Glu	Glu	Val	Glu
		115				120						125			
Phe	Ile	Ser	Val	Pro	Val	Pro	Glu	Phe	Ala	Asp	Ser	Asp	Pro	Ala	Asn
	130					135					140				
Ile	Val	His	Asp	Phe	Asn	Lys	Lys	Leu	Thr	Ala	Tyr	Leu	Asp	Leu	Asn
	145				150					155				160	
Leu	Asp	Lys	Cys	Tyr	Val	Ile	Pro	Leu	Asn	Thr	Ser	Ile	Val	Met	Pro
			165					170					175		
Pro	Arg	Asn	Leu	Leu	Glu	Leu	Leu	Ile	Asn	Ile	Lys	Ala	Gly	Thr	Tyr
		180						185					190		
Leu	Pro	Gln	Ser	Tyr	Leu	Ile	His	Glu	His	Met	Val	Ile	Thr	Asp	Arg
	195					200					205				
Ile	Glu	Asn	Ile	Asp	His	Leu	Gly	Phe	Phe	Ile	Tyr	Arg	Leu	Cys	His
	210				215					220					
Asp	Lys	Glu	Thr	Tyr	Lys	Leu	Gln	Arg	Arg	Glu	Thr	Ile	Lys	Gly	Ile
	225				230					235				240	
Gln	Lys	Arg	Glu	Ala	Ser	Asn	Cys	Phe	Ala	Ile	Arg	His	Phe	Glu	Asn
			245					250					255		
Lys	Phe	Ala	Val	Glu	Thr	Leu	Ile	Cys	Ser						
		260						265							

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```

Met Pro Thr Gly Asp Phe Asp Ser Lys Pro Ser Trp Ala Asp Gln Val
 1           5           10           15
Glu Glu Glu Gly Glu Asp Asp Lys Cys Val Thr Ser Glu Leu Leu Lys
          20           25           30
Gly Ile Pro Leu Ala Thr Gly Asp Thr Ser Pro Glu Pro Glu Leu Leu
          35           40           45
Pro Gly Ala Pro Leu Pro Pro Pro Lys Glu Val Ile Asn Gly Asn Ile
          50           55           60
Lys Thr Val Thr Glu Tyr Lys Ile Asp Glu Asp Gly Lys Lys Phe Lys
65           70           75           80
Ile Val Arg Thr Phe Arg Ile Glu Thr Arg Lys Ala Ser Lys Ala Val
          85           90           95
Ala Arg Arg Lys Asn Trp Lys Lys Phe Gly Asn Ser Glu Phe Asp Pro
          100          105          110
Pro Gly Pro Asn Val Ala Thr Thr Thr Val Ser Asp Asp Val Ser Met
          115          120          125
Thr Phe Ile Thr Ser Lys Glu Asp Leu Asn Cys Gln Glu Glu Asp
          130          135          140
Pro Met Asn Lys Phe Lys Gly Gln Lys Ile Val Ser Cys Arg Ile Cys
145          150          155          160
Lys Gly Asp His Trp Thr Thr Arg Cys Pro Tyr Lys Asp Thr Leu Gly
          165          170          175
Pro Met Gln Lys Glu Leu Ala Glu Gln Leu Gly Leu Ser Thr Gly Glu
          180          185          190
Lys Glu Lys Leu Pro Gly Glu Leu Glu Pro Val Gln Ala Thr Gln Asn
          195          200          205
Lys Thr Gly Lys Tyr Val Pro Pro Ser Leu Arg Asp Gly Ala Ser Arg
          210          215          220
Arg Gly Glu Ser Met Gln Pro Asn Arg Arg Ala Asp Asp Asn Ala Thr
225          230          235          240
Ile Arg Val Thr Asn Leu Arg Arg Gly His Ala
          245          250

```

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met Arg Arg Leu Asn Arg Lys Lys Thr Leu Ser Leu Val Lys Glu Leu

1	5	10	15
Asp	Ala	Phe	Pro
20	Lys	Val	Pro
Gly	Gly	Thr	Val
35	Ser	Leu	Ile
40	Ala	Phe	Thr
45	Thr	Thr	Met
50	Ile	Met	Glu
55	Phe	Ser	Val
60	Tyr	Gln	Asp
65	Thr	Trp	Met
70	Lys	Tyr	Glu
75	Ile	Asn	Ile
80	Asp	Val	Leu
85	Thr	Val	Ala
90	Met	Lys	Val
95	Ala	Glu	Thr
100	Met	Val	Ala
105	Ser	Ala	Asp
110	Gly	Leu	Val
115	Tyr	Glu	Pro
120	Thr	Gln	Arg
125	Met	Leu	Gln
130	Val	Ile	Asp
135	Thr	Ser	Leu
140	His	Glu	Glu
145	Thr	Ser	Thr
150	Ala	Leu	Pro
155	Arg	Ile	His
160	Gly	His	Leu
165	Thr	Val	Gly
170	Thr	Val	Gly
175	His	Val	Gly
180	His	Val	Gly
185	His	Val	Gly
190	His	Val	Gly
195	His	Val	Gly
200	His	Val	Gly
205	His	Val	Gly
210	His	Val	Gly
215	His	Val	Gly
220	His	Val	Gly
225	His	Val	Gly
230	His	Val	Gly
235	His	Val	Gly
240	His	Val	Gly
245	His	Val	Gly
250	His	Val	Gly
255	His	Val	Gly
260	His	Val	Gly
265	His	Val	Gly
270	His	Val	Gly
275	His	Val	Gly
280	His	Val	Gly
285	His	Val	Gly
290	His	Val	Gly
295	His	Val	Gly
300	His	Val	Gly
305	His	Val	Gly
310	His	Val	Gly
315	His	Val	Gly
320	His	Val	Gly
325	His	Val	Gly
330	His	Val	Gly
335	His	Val	Gly
340	His	Val	Gly
345	His	Val	Gly
350	His	Val	Gly
355	His	Val	Gly
360	His	Val	Gly
365	His	Val	Gly
370	His	Val	Gly
375	His	Val	Gly

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

Met Gly Ser Gln His Ser Ala Ala Ala Arg Pro Ser Ser Cys Arg Arg
 1           5           10           15
Lys Gln Glu Asp Asp Arg Asp Gly Leu Leu Ala Glu Arg Glu Gln Glu
           20           25           30
Glu Ala Ile Ala Gln Phe Pro Tyr Val Glu Phe Thr Gly Arg Asp Ser
           35           40           45
Ile Thr Cys Leu Thr Cys Gln Gly Thr Gly Tyr Ile Pro Thr Glu Gln
           50           55           60
Val Asn Glu Leu Val Ala Leu Ile Pro His Ser Asp Gln Arg Leu Arg
           65           70           75           80
Pro Gln Arg Thr Lys Gln Tyr Val Leu Leu Ser Ile Leu Leu Cys Leu
           85           90           95
Leu Ala Ser Gly Leu Val Val Phe Phe Leu Phe Pro His Ser Val Leu
           100          105          110
Val Asp Asp Asp Gly Ile Lys Val Val Lys Val Thr Phe Asn Lys Gln
           115          120          125
Asp Ser Leu Val Ile Leu Thr Ile Met Ala Thr Leu Lys Ile Arg Asn
           130          135          140
Ser Asn Phe Tyr Thr Val Ala Val Thr Ser Leu Ser Ser Gln Ile Gln
           145          150          155          160
Tyr Met Asn Thr Val Val Ser Thr Tyr Val Thr Thr Asn Val Ser Leu
           165          170          175
Ile Pro Pro Arg Ser Glu Gln Leu Val Asn Phe Thr Gly Lys Ala Glu
           180          185          190
Met Gly Gly Pro Phe Ser Tyr Val Tyr Phe Phe Cys Thr Val Pro Glu
           195          200          205
Ile Leu Val His Asn Ile Val Ile Phe Met Arg Thr Ser Val Lys Ile
           210          215          220
Ser Tyr Ile Gly Leu Met Thr Gln Ser Ser Leu Glu Thr His His Tyr
           225          230          235          240
Val Asp Cys Gly Gly Asn Ser Thr Ala Ile
           245          250

```

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```

Met Val Thr Cys Phe His Val Pro Tyr Ser Ala Leu Thr Met Phe Ile
 1           5           10           15
Ser Thr Glu Gln Thr Glu Arg Asp Ser Ala Thr Ala Tyr Arg Met Thr
           20           25           30
Val Glu Val Leu Gly Thr Val Leu Gly Thr Ala Ile Gln Gly Gln Ile
           35           40           45
Val Gly Gln Ala Asp Thr Pro Cys Phe Gln Asp Leu Asn Ser Ser Thr
           50           55           60
Val Ala Ser Gln Ser Ala Asn His Thr His Gly Thr Thr Ser His Arg

```

```

65          70          75          80
Glu Thr Gln Lys Ala Tyr Leu Leu Ala Ala Gly Val Ile Val Cys Ile
          85          90          95
Tyr Ile Ile Cys Ala Val Ile Leu Ile Leu Gly Val Arg Glu Gln Arg
          100          105          110
Glu Pro Tyr Glu Ala Gln Gln Ser Glu Pro Ile Ala Tyr Phe Arg Gly
          115          120          125
Leu Arg Leu Val Met Ser His Gly Pro Tyr Ile Lys Leu Ile Thr Gly
          130          135          140
Phe Leu Phe Thr Ser Leu Ala Phe Met Leu Val Glu Gly Asn Phe Val
          145          150          155          160
Leu Phe Cys Thr Tyr Thr Leu Gly Phe Arg Asn Glu Phe Gln Asn Leu
          165          170          175
Leu Leu Ala Ile Met Leu Ser Ala Thr Leu Thr Ile Pro Ile Trp Gln
          180          185          190
Trp Phe Leu Thr Arg Phe Gly Lys Lys Thr Ala Val Tyr Val Gly Ile
          195          200          205
Ser Ser Ala Val Pro Phe Leu Ile Leu Val Ala Leu Met Glu Ser Asn
          210          215          220
Leu Ile Ile Thr Tyr Ala Val Ala Val Ala Ala Gly Ile Ser Val Ala
          225          230          235          240
Ala Ala Phe Leu Leu Pro Trp Ser Met Leu Pro Asp Val Ile Asp Asp
          245          250          255
Phe His Leu Lys Gln Pro His Phe His Gly Thr Glu Pro Ile Phe Phe
          260          265          270
Ser Phe Tyr Val Phe Phe Thr Lys Phe Ala Ser Gly Val Ser Leu Gly
          275          280          285
Ile Ser Thr Leu Ser Leu Asp Phe Ala Gly Tyr Gln Thr Arg Gly Cys
          290          295          300
Ser Gln Pro Glu Arg Val Lys Phe Thr Leu Asn Met Leu Val Thr Met
          305          310          315          320
Ala Pro Ile Val Leu Ile Leu Leu Gly Leu Leu Leu Phe Lys Met Tyr
          325          330          335
Pro Ile Asp Glu Glu Arg Arg Arg Gln Asn Lys Lys Ala Leu Gln Ala
          340          345          350
Leu Arg Asp Glu Ala Ser Ser Ser Gly Cys Ser Glu Thr Asp Ser Thr
          355          360          365
Glu Leu Ala Ser Ile Leu
          370

```

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```

Met Val Asn Asp Pro Pro Val Pro Ala Leu Leu Trp Ala Gln Glu Val
1          5          10          15
Gly Gln Val Leu Ala Gly Arg Ala Arg Arg Leu Leu Leu Gln Phe Gly
          20          25          30
Val Leu Phe Cys Thr Ile Leu Leu Leu Leu Trp Val Ser Val Phe Leu

```

```

      35              40              45
Tyr Gly Ser Phe Tyr Tyr Ser Tyr Met Pro Thr Val Ser His Leu Ser
  50              55              60
Pro Val His Phe Tyr Tyr Arg Thr Asp Cys Asp Ser Ser Thr Thr Ser
  65              70              75              80
Leu Cys Ser Phe Pro Val Ala Asn Val Ser Leu Thr Lys Gly Gly Arg
      85              90              95
Asp Arg Val Leu Met Tyr Gly Gln Pro Tyr Arg Val Thr Leu Glu Leu
      100              105              110
Glu Leu Pro Glu Ser Pro Val Asn Gln Asp Leu Gly Met Phe Leu Val
      115              120              125
Thr Ile Ser Cys Tyr Thr Arg Gly Gly Arg Ile Ile Ser Thr Ser Ser
      130              135              140
Arg Ser Val Met Leu His Tyr Arg Ser Asp Leu Leu Gln Met Leu Asp
      145              150              155              160
Thr Leu Val Phe Ser Ser Leu Leu Leu Phe Gly Phe Ala Glu Gln Lys
      165              170              175
Gln Leu Leu Glu Val Glu Leu Tyr Ala Asp Tyr Arg Glu Asn Ser Tyr
      180              185              190
Val Pro Thr Thr Gly Ala Ile Ile Glu Ile His Ser Lys Arg Ile Gln
      195              200              205
Leu Tyr Gly Ala Tyr Leu Arg Ile His Ala His Phe Thr Gly Leu Arg
      210              215              220
Tyr Leu Leu Tyr Asn Phe Pro Met Thr Cys Ala Phe Ile Gly Val Ala
      225              230              235              240
Ser Asn Phe Thr Phe Leu Ser Val Ile Val Leu Phe Ser Tyr Met Gln
      245              250              255
Trp Val Trp Gly Gly Ile Trp Pro Arg His Arg Phe Ser Leu Gln Val
      260              265              270
Asn Ile Arg Lys Arg Asp Asn Ser Arg Lys Glu Val Gln Arg Arg Ile
      275              280              285
Ser Ala His Gln Pro Gly Pro Glu Gly Gln Glu Glu Ser Thr Pro Gln
      290              295              300
Ser Asp Val Thr Glu Asp Gly Glu Ser Pro Glu Asp Pro Ser Gly Thr
      305              310              315              320
Glu Val Ser Cys Pro Arg Arg Arg Asn Gln Ile Ser Ser Pro
      325              330

```

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```

Met Thr His Pro Gly Thr Gly Asp Ile Ile Ala Val Met Ile Thr Glu
  1              5              10              15
Leu Arg Gly Lys Asp Ile Leu Ser Tyr Leu Glu Lys Asn Ile Ser Val
      20              25              30
Gln Met Thr Ile Ala Val Gly Thr Arg Met Pro Pro Lys Asn Phe Ser
      35              40              45
Arg Gly Ser Leu Val Phe Val Ser Ile Ser Phe Ile Val Leu Met Ile

```

```

      50              55              60
Ile Ser Ser Ala Trp Leu Ile Phe Tyr Phe Ile Gln Lys Ile Arg Tyr
65              70              75              80
Thr Asn Ala Arg Asp Arg Asn Gln Arg Arg Leu Gly Asp Ala Ala Lys
      85              90              95
Lys Ala Ile Ser Lys Leu Thr Thr Arg Thr Val Lys Lys Gly Asp Lys
      100              105              110
Glu Thr Asp Pro Asp Phe Asp His Cys Ala Val Cys Ile Glu Ser Tyr
      115              120              125
Lys Gln Asn Asp Val Val Arg Ile Leu Pro Cys Lys His Val Phe His
      130              135              140
Lys Ser Cys Val Asp Pro Trp Leu Ser Glu His Cys Thr Cys Pro Met
145              150              155              160
Cys Lys Leu Asn Ile Leu Lys Ala Leu Gly Ile Val Pro Asn Leu Pro
      165              170              175
Cys Thr Asp Asn Val Ala Phe Asp Met Glu Arg Leu Thr Arg Thr Gln
      180              185              190
Ala Val Asn Arg Arg Ser Ala Leu Gly Asp Leu Ala Gly Asp Asn Ser
      195              200              205
Leu Gly Leu Glu Pro Leu Arg Thr Ser Gly Ile Ser Pro Leu Pro Gln
      210              215              220
Asp Gly Glu Leu Thr Pro Arg Thr Gly Glu Ile Asn Ile Ala Val Thr
225              230              235              240
Lys Glu Trp Phe Ile Ile Ala Ser Phe Gly Leu Leu Ser Ala Leu Thr
      245              250              255
Leu Cys Tyr Met Ile Ile Arg Ala Thr Ala Ser Leu Asn Ala Asn Glu
      260              265              270
Val Glu Trp Phe
      275

```

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```

Met Ala Asn Ser Gly Leu Gln Leu Leu Gly Phe Ser Met Ala Leu Leu
 1              5              10              15
Gly Trp Val Gly Leu Val Ala Cys Thr Ala Ile Pro Gln Trp Gln Met
      20              25              30
Ser Ser Tyr Ala Gly Asp Asn Ile Thr Ala Gln Ala Met Tyr Lys
      35              40              45
Gly Leu Trp Met Asp Cys Val Thr Gln Ser Thr Gly Met Met Ser Cys
      50              55              60
Lys Met Tyr Asp Ser Val Leu Ala Leu Ser Ala Ala Leu Gln Ala Thr
      65              70              75              80
Arg Ala Leu Met Val Val Ser Leu Val Leu Gly Phe Leu Ala Met Phe
      85              90              95
Val Ala Thr Met Gly Met Lys Cys Thr Arg Cys Gly Gly Asp Asp Lys
      100              105              110
Val Lys Lys Ala Arg Ile Ala Met Gly Gly Gly Ile Ile Phe Ile Val

```

```

      115              120              125
Ala Gly Leu Ala Ala Leu Val Ala Cys Ser Trp Tyr Gly His Gln Ile
      130              135              140
Val Thr Asp Phe Tyr Asn Pro Leu Ile Pro Thr Asn Ile Lys Tyr Glu
      145              150              155              160
Phe Gly Pro Ala Ile Phe Ile Gly Trp Ala Gly Ser Ala Leu Val Ile
      165              170              175
Leu Gly Gly Ala Leu Leu Ser Cys Ser Cys Pro Gly Asn Glu Ser Lys
      180              185              190
Ala Gly Tyr Arg Ala Pro Arg Ser Tyr Pro Lys Ser Asn Ser Ser Lys
      195              200              205
Glu Tyr
      210

```

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```

Met Ile Arg Pro Gln Leu Arg Thr Ala Gly Leu Gly Arg Cys Leu Leu
 1           5           10           15
Pro Gly Leu Leu Leu Leu Val Pro Val Leu Trp Ala Gly Ala Glu
      20           25           30
Lys Leu His Thr Gln Pro Ser Cys Pro Ala Val Cys Gln Pro Thr Arg
      35           40           45
Cys Pro Ala Leu Pro Thr Cys Ala Leu Gly Thr Thr Pro Val Phe Asp
      50           55           60
Leu Cys Arg Cys Cys Arg Val Cys Pro Ala Ala Glu Arg Glu Val Cys
      65           70           75           80
Gly Gly Ala Gln Gly Gln Pro Cys Ala Pro Gly Leu Gln Cys Leu Gln
      85           90           95
Pro Leu Arg Pro Gly Phe Pro Ser Thr Cys Gly Cys Pro Thr Leu Gly
      100          105          110
Gly Ala Val Cys Gly Ser Asp Arg Arg Thr Tyr Pro Ser Met Cys Ala
      115          120          125
Leu Arg Ala Glu Asn Arg Ala Ala Arg Arg Leu Gly Lys Val Pro Ala
      130          135          140
Val Pro Val Gln Trp Gly Asn Cys Gly Asp Thr Gly Thr Arg Ser Ala
      145          150          155          160
Gly Pro Leu Arg Arg Asn Tyr Asn Phe Ile Ala Ala Val Val Glu Lys
      165          170          175
Val Ala Pro Ser Val Val His Val Gln Leu Trp Gly Arg Leu Leu His
      180          185          190
Gly Ser Arg Leu Val Pro Val Tyr Ser Gly Ser Gly Phe Ile Val Ser
      195          200          205
Glu Asp Gly Leu Ile Ile Thr Asn Ala His Val Val Arg Asn Gln Gln
      210          215          220
Trp Ile Glu Val Val Leu Gln Asn Gly Ala Arg Tyr Glu Ala Val Val
      225          230          235          240
Lys Asp Ile Asp Leu Lys Leu Asp Leu Ala Val Ile Lys Ile Glu Ser

```

[illegible]

(A) LENGTH: 266 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met	Val	Lys	Val	Thr	Phe	Asn	Ser	Ala	Leu	Ala	Gln	Lys	Glu	Ala	Lys
1				5					10					15	
Lys	Asp	Glu	Pro	Glu	Ser	Gly	Glu	Glu	Ala	Leu	Ile	Ile	Pro	Pro	Asp
			20					25					30		
Ala	Val	Ala	Val	Asp	Cys	Lys	Asp	Pro	Asp	Asp	Val	Val	Pro	Val	Gly
		35					40					45			
Gln	Arg	Arg	Ala	Trp	Cys	Trp	Cys	Met	Cys	Phe	Gly	Leu	Ala	Phe	Met
	50					55					60				
Leu	Ala	Gly	Val	Ile	Leu	Gly	Gly	Ala	Tyr	Leu	Tyr	Lys	Tyr	Phe	Ala
65				70					75						80
Leu	Gln	Pro	Asp	Asp	Val	Tyr	Tyr	Cys	Gly	Ile	Lys	Tyr	Ile	Lys	Asp
				85					90					95	
Asp	Val	Ile	Leu	Asn	Glu	Pro	Ser	Ala	Asp	Ala	Pro	Ala	Ala	Leu	Tyr
			100					105					110		
Gln	Thr	Ile	Glu	Glu	Asn	Ile	Lys	Ile	Phe	Glu	Glu	Glu	Glu	Val	Glu

	115		120		125
Phe	Ile Ser Val Pro Val	Pro Glu Phe Ala Asp	Ser Asp Pro Ala Asn		
130		135	140		
Ile Val His Asp Phe Asn	Lys Lys Leu Thr Ala Tyr	Leu Asp Leu Asn			
145		150	155		160
Leu Asp Lys Cys Tyr Val	Ile Pro Leu Asn Thr Ser	Ile Val Met Pro			
	165	170	175		
Pro Arg Asn Leu Leu Glu	Leu Ile Asn Ile Lys Ala Gly Thr Tyr				
	180	185	190		
Leu Pro Gln Ser Tyr Leu	Ile His Glu His Met Val	Ile Thr Asp Arg			
	195	200	205		
Ile Glu Asn Ile Asp His	Leu Gly Phe Phe Ile Tyr Arg	Leu Cys His			
210		215	220		
Asp Lys Glu Thr Tyr Lys	Leu Gln Arg Arg Glu Thr	Ile Lys Gly Ile			
225		230	235		240
Gln Lys Arg Glu Ala Ser	Asn Cys Phe Ala Ile Arg	His Phe Glu Asn			
	245	250	255		
Lys Phe Ala Val Glu Thr	Leu Ile Cys Ser				
	260	265			

115
 130
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